

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problems Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2001, 11:00:46 ; Search time 21.1 Seconds
(without alignments) updates/sec
3032.541 Million cell

Title: US-09-587-574-1

Perfect score: 4445

Sequence: 1 MSSAVLVTLPLPDPSSSFRED.....DETVLPMYEGRIIGKVERID 840

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4310	97.0	838	2 T08423	Axin homolog Axil
2	1661	37.4	832	2 T08422	negative regulator
3	190.5	4.3	544	2 UC5503	G-protein signalin
4	189.5	4.3	519	2 S78089	G-protein signalin
5	173.5	3.9	1510	2 T33100	hypothetical prote
6	172.5	3.9	211	2 I53020	G-0/G-1 switch reg
7	167	3.8	173	2 S71812	RG510 protein - hu
8	163.5	3.7	533	2 T31002	hypothetical prote
9	161.5	3.6	181	2 UC7228	G-protein signalin
10	159	3.6	196	2 S43436	B cell activation
11	157.5	3.5	205	2 S78221	G-protein signalin
12	153.5	3.5	1023	2 T31669	neural zinc finger
13	151.5	3.4	1618	2 S21424	nestin - human
14	151	3.4	1150	2 S56775	myt1 protein - smu
15	150	3.4	1032	2 T14124	neural zinc finger
16	149	3.4	2559	2 T09144	probable guanine n
17	148	3.3	1791	2 T02345	hypothetical prote
18	147	3.3	1200	2 A46194	neurofilament prot
19	143.5	3.2	1213	2 A58198	serine/proline-ric
20	143.5	3.2	1272	2 T30248	fragile X mental r
21	143.5	3.2	2416	2 T13825	adenomatous polyo
22	143	3.2	1383	2 T13052	guanine nucleotide
23	142.5	3.2	455	2 I48724	zinc finger protei
24	142.5	3.2	1210	2 T39410	AF-4 protein, spli
25	141	3.2	997	2 T28872	hypothetical prote
26	140	3.1	1677	2 T14267	hypothetical prote
27	139	3.1	284	2 T15700	hypothetical prote
28	138.5	3.1	1403	2 S24548	homeotic protein P
29	137	3.1	2688	2 I49477	alpha-A-crystallin

30	136.5	3.1	814	2 T26702	hypothetical prote
31	136.5	3.1	2464	1 ORWSP1	microtubule-associ
32	136	3.1	1634	2 T26517	hypothetical prote
33	136	3.1	1655	2 T32633	hypothetical prote
34	135.5	3.0	1234	2 T30160	hypothetical prote
35	135.5	3.0	1507	2 B47328	natural killer cel
36	135.5	3.0	2298	2 T49648	hypothetical prote
37	134.5	3.0	1736	2 T00391	hypothetical prote
38	134.5	3.0	2722	2 T20532	hypothetical prote
39	134.5	3.0	3942	2 T42730	Basoon protein -
40	133.5	3.0	3924	2 S37431	ankyrin 2, neurona
41	132.5	3.0	1166	2 T13958	synGAP-b1 protein
42	132.5	3.0	1249	2 T14270	Ras-GTPase activat
43	132.5	3.0	1293	2 T14259	Ras-GTPase activat
44	132.5	3.0	1585	2 T31611	hypothetical prote
45	132.5	3.0	1983	2 T00385	KIAA0624 protein -

ALIGNMENTS

RESULT 1
T08423
Axin homolog Axil - rat
N:Alternate names: Axil
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T08423
R:Yamamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, M.; Cell. Biol. 18, 2867-2875, 1998
A:Title: Axil, a member of the Axin family, interacts with both glycogen synthase kin
A:Reference number: 216414; MUID:98226558
A:Accession: T08423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-838 <YAM>
A:Cross-References: EMBL:AF017757; NID:93080758; PIDN:AAC40089.1; PID:93080759
A:Note: interacts with GSK-3beta and beta-catenin
C:Keywords: phosphoprotein; signal transduction

Query Match	Score	DB 2:	Length	838:
Best Local Similarity	96.9%	Pred. No. 9.3e-265;		
Matches	814;	Conservative	7;	Mismatches 17; Indels 2; Gaps 1;
QY	1	MSSAVLVTLPLPDPSSSFREDAPPPVPGEGETPPCQPSYGVKQSTKPMVSSNARNRD	60	
DB	1	MSSAVLVTLPLPDPSSSFREDAPPPVPGEGETPPCQPSYGVKQSTKPMVSSNARNRD	60	
QY	61	GIIEPEGRASPPSPILRMTKSLHSILGDODGAYLPTFLEREKCVDTLDFWFACNGFFROM	120	
DB	61	GIIEPEGRASPPSPILRMTKSLHSILGDODGAYLPTFLEREKCVDTLDFWFACNGFFROM	120	
QY	121	NLKDTFLVANAAYRYIENNSVSKOLKPAKTYIRDGIRKQOIGSVMPDQAGTEIQA	180	
DB	121	NLKDTFLVANAAYRYIENNSVSKOLKPAKTYIRDGIRKQOIGSVMPDQAGTEIQA	180	
QY	181	VNEENAYQFLTSDIYLEVRSRGENTAYMSNGCLSLKVLGAYLPTLNEEBEWTCADLK	240	
DB	181	VNEENAYQFLTSDIYLEVRSRGENTAYMSNGCLSLKVLGAYLPTLNEEBEWTCADLK	240	
QY	241	CKLSPVVLGSKTLRATASVSTETAEENGFRSKSDVNPVHVGSGVFPAPATSANDS	300	
DB	241	CKLSPVVLGSKTLRATASVSTETAEENGFRSKSDVNPVHVGSGVFPAPATSANDS	300	
QY	301	ELSSDALTDSDSMTDSSVDGVPYRMGSKQLOREMHRSVYKANGOVSLPHFPRTRLPK	360	
DB	301	ELSSDALTDSDSMTDSSVDGIPYRMGSKQLOREMHRSVYKANGOVSLPHFPRTRLPK	360	
QY	361	EMTPVEPAAPAAELISRLKLELESRLSLEERLOQIREDEKESGSDALSRDCAPOVQ	420	
DB	361	EMTPVEPAAPAAELISRLKLELESRLSLEERLOQIREDEKESGSDALSRDCAPOVQ	420	

Query Match 3.5%; Score 153.5; DB 2; Length 1023;
 Best Local Similarity 20.7%; Pred. No. 0.097;
 Matches 152; Conservative 82; Mismatches 230; Indels 271; Gaps 38;

198 EYVRSNGENTAWMSNGIGSLKGLYLPTLNEEEMTCADLKCKLSPYVGLSKTLRA 257
 Db 119 ESVQTVGEN---LNGNGIQLKAEK-----DEANE-----CM-----148

258 TASVASTETANGFSPFRSDPVNPNYHVGSGYVAPATSAANDSELSDALTDSSKMTDS 317
 Db 149 -----HSDGDRKVNHSQ-----PFCSSGDSSESDNTENGWGSNS 188

318 SVDGVPYRMSKKOL---OREMNR---SVKANGVSLPHFRTLRLEMPVPEAPAA 372
 Db 189 SED---TDHKKPKRKLTYNKKDLLEVPIKABD---KFCENKCDSDTSGRPQNSHM 243

373 ELIS-RLEKLELESRHSLEERLQIREDEKESG---EQ--ALSSRDGAPVQHPLAL 425
 Db 244 EPLSVKVPSPFEVEESESATVIAESAIEVKKAKGSLSLQALALQAEKSGVFHH-----299

426 LPSGSEEDPOTIIDHLSRYLKTGCGSPGVGR-----YSPRSRSDPHHHQHNNHQC 479
 Db 300 -----TYKELDRFL-DHLAROROPKV-TDASGRQIFNNKHSPPR---PERRE-----342

480 HTLLSTGKLRPVACPLLGKSFLLKQTKVHHNHVYIHHNAP-----KTEKEIEAETQ 535
 Db 343 -----AKCPILPGCGD-----TGHVGLYRHHNSLSGCHKAVVPLEITAMH 383

536 RVRLCPGCGTDYCYCKSKSHPKARPELPGEQFGSGGGLPKRNAGTEGIALSARDG 595
 Db 384 ENVLKLC-----PTPG---CTGRGHVNSNRNTHRSLSGCPITAAEK 420

596 -----GMSAAGCPOLPGEGDRSDPYWQ-----WMLESRSKSKPH-----633
 Db 421 LAMTQDSOLDSSOTGGP---EQAHVNLVKOIEFNPSQAITSPRASASKOEKFTGK 476

634 -----SAQSTRKSPLESARA--APGERVSRHH-----LLGASGHSKSVARAH 674
 Db 477 VPEDYASPDQAVFGRKRLDTGGQCKAPRPESKHFNSPKNGLPSAGAHQSTVIRAS 536

675 -----PTQDPAMPRLPPPTLQLEACRRLAEV--SKQOKORCCVASOORBN-----722
 Db 537 SYGHQVSED---THIAAAAILNLSTRCKEADTDLISNKPQSLRAKAELEVENGTLDL 593

723 -----HSAAGQAGASFPANPSIAP-----741
 Db 594 SMKNNRILDKSIGTSHTTIATPSSSPFKASSLLVNAFYALCDQEGNNVPIINYSKH 653

742 ---EDHKEPKKLASVHALQASELVYFFCGE-EIP-----YRMLKAQSLTL-----785
 Db 654 GKTEEEKKDPVNSLENLEKK-----FAGEASIPSPKPLHTRLDKLKLICPTPGCD 707

786 ---GHFKQSLSKKNY 798
 Db 708 GSGHV-----TGNV 716

RESULT 13
 S21424
 nestin - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C:Accession: S21424
 R:Dahtstrand, J.; McKay, R.D.G.; Zimmerman, L.B.; Lendahl, U.
 submitted to the EMBL Data Library, May 1992
 A:Description: Characterization of the human nestin gene reveals a close evolutionary re
 A:Reference number: S21424
 A:Accession: S21424
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1618 <DAH>

A:Cross-references: EMBL:X65964; NID:935018; PIDN:CAA46780.1; PID:935019

Query Match 3.4%; Score 151.5; DB 2; Length 1618;
 Best Local Similarity 19.4%; Pred. No. 0.25;
 Matches 180; Conservative 108; Mismatches 333; Indels 309; Gaps 42;

21 APPRVGE-EGETPP---CQPSVKVQSTKPM-----PYSSNARNRNDG 61
 Db 395 APSPAVAELIADAPLSLQTOGGRQADPEPLRAEARVAIPASVLRPPEPGQREQEAS 454

62 LGE-PEGASPDSPILTWTSLSHSLGDQGAIFYFR-----FLEREKVDTLD 109
 Db 455 TGQSPEDHASIAPPLSDHSHLEKQDESGSRYFSICREGEQGLWGLKEFTALEEG--512

110 FWFACNGFRQMLKDTLTKLRAKAIFYRYIENNSVSKOLKPAIKTYIRDGIRKQOIGSV 169
 Db 513 -----KVSSLSQEIWEEDLANKELQDQVPLEKETLK--SLGEE 551

170 MFQDAQTEIQAVMEENAYQVF-----LTSDIYLEVRS-----GGEPT 207
 Db 552 IQESLKT---LENQSHETLERENQCPRLSEED--LETLKSLERENKRAIKCGGSET 604

208 AYMSNGIGSLKYLKGLYPLTNEEEMTCADLK---CKLSPTVVG-LSSKTLATASVRS 263
 Db 605 -----SRKGCRLKPTGKEDDTYOTLOSLOKENDOLKMSLEGNLETFLEPGTENQEL 655

264 TETAENGFRSF-----KRSDPVNPNYHVGSGYVAPATSAANDSELSDALTD-----310
 Db 656 VSSLOENLESLTALERENQEPRLSPREVGDEALRPILTKENQBLRS--LEDEKKAFRSL 713

311 -----SMTDSSVDGVPVRYRMSKKOLQ-----REHNRVYKAN 344
 Db 714 EKENEQPKLLEEDDSI--VRPLETNHKSLSLEBODETLRLTEKETQOORRSLGQ 771

345 GQVSLPHFPRTNRLPKEMTPVPEAPAAELISR-----LEKLE-LESRHSLEER 394
 Db 772 DQMTL-----RPEKVDLEPLKSLDOELARPLENNOEFLKSLKESVAVKSLTE 823

395 LQOIRDEKESQALSSRDGAPVQHPLALPBGSEEDPQ-----TLDHLSVLYKT 449
 Db 824 ILESLSAQOENLETIKSPETOAPLMTPEINKSGNESSRKONSHTTVCSEPERDIOT 883

450 PGQSGPV---GRVSPR---SRSPDHHQNH-----HHQOCHTLSTGKLP 490
 Db 884 PGRGEGIIIEISGMRGEFEISRGVDKESQRLLEENLKGGEYQESLRSLEEGQELP 943

491 PVA-----ACPLIG-----KSFLLTKQTKVHHNHVYH 518
 Db 944 QSADVQRMEDTVEKQDELQAESPPGMAGVENKDEALNLRDQDFTGKE-----992

519 HHAIVPTKEIELEAMQORRCLOPGTDYCYCKSKSHKAPRELPGEQFGSGRGTLPK 578
 Db 993 -----EVDQGLNATEEV--WPPG-----EGHNEPEP-----KEQGLVEG 1028

579 RNAKTEPGIALSARDGMSAAGCPOLPGEGDRSDQVWQWMLSERSKSKPSPAOSI 638
 Db 1029 ASYKGAEGSL---QDPEGSOQVGTGLOAPG-----LPPAIE--1064

639 KKSYPLESARAP--GERVSRHHLGAS--GHSRSVARAP-----FTQDPAM 682
 Db 1065 ---PLVEDVAPRGDDQASPEYMLGSEPPAMGESAGAERGIGQVGGGLDPCHLRLREVM 1120

683 -PPLTPPNTLAQ-----LEACRRLAEVSK--PQOKORCCVASOORBNHSA--726
 Db 1121 EPLLEESLEARVQGLEGRPKDLGAGGLGTFSELPKSGSHDWPPEPREGRESEAEAP 1180

727 -GQAGASFPANSLAPEDHKPEPKLASVHA 755
 Db 1181 RGAEEAFPAETLGHGSDAPSPWPLGSEEA 1210

RESULT 14

Tue Oct 23 15:36:23 2001

us-09-587-574-1.rpt

Page 8

Search completed: October 23, 2001, 11:03:18
Job time: 152 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2001, 11:00:11 ; Search time 13.99 Seconds
(without alignments)
1236.304 Million cell updates/sec

Title: US-09-587-574-1

Perfect score: 4445
Sequence: 1 MSSAVLVTLPPDPSSSFRED.....DETVLPMYEGRIIGKVERID 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Match	Length	ID	Description
- No.					
1	172.5	3.9	211	2	US-08-748-483-4
2	170.5	3.8	243	2	US-08-829-110-3
3	166	3.7	119	2	US-08-588-258B-31
4	166	3.7	119	3	US-08-460-505-31
5	166	3.7	119	5	PCT-US96-08295-31
6	166	3.7	196	2	US-08-829-110-5
7	166	3.7	196	2	US-08-748-483-3
8	162.5	3.7	1182	4	US-09-041-886-21
9	159	3.6	181	2	US-08-748-483-1
10	158	3.6	121	2	US-08-588-258B-32
11	158	3.6	121	3	US-08-460-505-32
12	158	3.6	121	5	PCT-US96-08295-32
13	157.5	3.5	205	2	US-08-829-110-6
14	157.5	3.5	205	2	US-08-748-483-5
15	152	3.4	159	2	US-08-829-110-1
16	151.5	3.4	1618	1	US-07-853-913-4
17	149	3.4	2509	2	US-08-149-097D-35
18	146.5	3.3	202	1	US-08-274-318-2
19	146.5	3.3	202	2	US-08-463-081B-2
20	146.5	3.3	202	2	US-08-461-379A-2
21	146.5	3.3	202	2	US-08-462-390B-2
22	146.5	3.3	202	2	US-08-754-108-2
23	146.5	3.3	202	3	US-08-870-815-4
24	146.5	3.3	202	3	US-08-463-074B-2
25	146.5	3.3	202	3	US-08-465-585C-2
26	146.5	3.3	202	3	US-08-652-446-2
27	146.5	3.3	202	4	US-08-949-004-4

28	146.5	3.3	570	3	US-08-826-246-2	Sequence 2, Appl
29	146.5	3.3	570	3	US-08-944-495-2	Sequence 2, Appl
30	146.5	3.3	570	3	US-09-126-640-7	Sequence 7, Appl
31	146.5	3.3	570	4	US-08-925-588-2	Sequence 2, Appl
32	143.5	3.2	201	2	US-08-726-228-2	Sequence 2, Appl
33	143.5	3.2	201	3	US-08-870-815-2	Sequence 2, Appl
34	143.5	3.2	201	4	US-08-949-004-2	Sequence 2, Appl
35	142.5	3.2	1187	2	US-08-320-559-28	Sequence 28, Appl
36	142.5	3.2	1187	3	US-08-545-860D-28	Sequence 28, Appl
37	142.5	3.2	1187	5	PCT-US94-04496-28	Sequence 26, Appl
38	142.5	3.2	1210	1	US-08-320-559-26	Sequence 26, Appl
39	142.5	3.2	1210	5	US-08-545-860D-26	Sequence 26, Appl
40	142.5	3.2	1210	5	PCT-US94-04496-26	Sequence 26, Appl
41	135	3.0	123	2	US-08-588-258B-39	Sequence 39, Appl
42	135	3.0	123	5	PCT-US96-08295-39	Sequence 39, Appl
43	131.5	3.0	2441	1	US-08-194-468-2	Sequence 2, Appl
44	131.5	3.0	2441	3	US-08-961-739-2	Sequence 2, Appl
45	128.5	2.9	763	4	US-08-961-083-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-08-748-483-4
Sequence 4, Application US/08748483
Patent No. 5955314
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,483
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0157 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 292037
US-08-748-483-4
Query Match 3.9%; Score 172.5; DB 2; Length 211;
Best Local Similarity 26.9%; Pred. No. 1.3e-07;

RESULT 4
US-08-460-505-31
; Sequence 31, Application US/08460505

Patent No. 6069296
GENERAL INFORMATION:
APPLICANT: Horvitz, Robert H.
APPLICANT: Koelle, Michael
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,505
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/214001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-505-31

Query Match 3.7%; Score 166; DB 3; Length 119;
Best Local Similarity 32.5%; Pred. No. 1.9e-07;
Matches 40; Conservative 29; Mismatches 46; Indels 8; Gaps 3;

QY 77 RWTGSHSLGDDGAYLERTFLERKCVDTLDPFACNGFR--QNLKDTTLRAKAI 134
DB 1 QWSQSLKRLAQTQNVGSLKSESENFELWACEDYKTESDLPCK---AEEI 56
QY 135 YKRYIENNSVSKQLPATKTYIRDGIRKQIGSVFDPQAGTEIQVMEENAYQVFLTSD 194
DB 57 YKAFVHSDA--AKQINIDRTRESTAKKIKAPPTPCFDEAKQVITYITLMKDSYPRLKSD 114
QY 195 IYL 197
DB 115 IYL 117

RESULT 5
PCT-US96-08295-31
Sequence 31, Application PC/TUS9608295
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALING
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08295
FILING DATE: 31-MAY-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,258
FILING DATE: 12-JAN-96
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/216001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-08295-31

Query Match 3.7%; Score 166; DB 5; Length 119;
Best Local Similarity 32.5%; Pred. No. 1.9e-07;
Matches 40; Conservative 29; Mismatches 46; Indels 8; Gaps 3;

QY 77 RWTGSHSLGDDGAYLERTFLERKCVDTLDPFACNGFR--QNLKDTTLRAKAI 134
DB 1 QWSQSLKRLAQTQNVGSLKSESENFELWACEDYKTESDLPCK---AEEI 56
QY 135 YKRYIENNSVSKQLPATKTYIRDGIRKQIGSVFDPQAGTEIQVMEENAYQVFLTSD 194
DB 57 YKAFVHSDA--AKQINIDRTRESTAKKIKAPPTPCFDEAKQVITYITLMKDSYPRLKSD 114
QY 195 IYL 197
DB 115 IYL 117

RESULT 6
US-08-829-110-5
Sequence 5, Application US/08829110
Patent No. 5882890
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,110
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

```
.Query Match      3.7%; Score 162.5; DB 4; Length 1182;
```

Best Local Similarity 21.1%; Pred. No. 1.8e-05;
Matches 102; Conservative 49; Mismatches 177; Indels 155; Gaps 21;

```

OY 274 FRRSDVPVPIHGS-GYFAPAT-----ANDSEL--SSDALTDSDSM-----IDS 317
DB 676 FORMPRPPTDGGGQNALPSTQDPCGALMAHESGLKESPSWYTORAQEFOKGTWS 735
OY 318 SYDGVPRYRMGSKQLO-----REMHRS-----VKANGQ---VSLPFRTHLPKEM 362
DB 736 PEGGPRTPMNPNSQSVEMKEMRGDGYSDSEHILPMEGGCRASMPRLPAENOTISPT 795
OY 363 TPVEPAFAELISR-----LEKLELESNLSLEERLQITREDEKEGSEQALSSRDG 416
DB 796 SPMKRSASVLGPKARLLDYSLERVPRENGR-----HQRRRDRSHRASRSL----- 844
OY 417 APVOHRLALLPBGSYEDRPTQLDDHLSNVLKTPGCGQSGVGRYSPRSPRHNNQHNNH 476
DB 845 -----GRY-TVDVGLGTDLG--MTQSGDLPSKERDGERGPRKRRKHROHHN 889
OY 477 QOCHTLSTGKLPVACRPLGKSFLLKQTKHNNHNNHNNHNNHNNHNNHNNHNNHNNHNNH 536
DB 890 -----NNNN-NHNNPRPKDYADERRDH 912
OY 537 VNCICPGTDDYCYCKSKSHPAKAPRLPGEOFGSRGCTLPRNAKGTERRGLALSARDG 596
DB 913 GR-----ARADQKWSRSPSEKREHMAHROGS-----SSVSGSPASTSGT 953
OY 597 MSSAGGQPLP-----GEGDRSDQVWOMLESEKOSKRP-HSQO 636
DB 954 STPRGRGRQLPQTPSTPRPHVSYSPVIRKAGSGPRPOO--QOQOQOQOQOQAVARGRKAT 1011
OY 637 STKRSYPLESAAARGERYSRHLLGASGHSRVARAHFTDPRMPLTPRNTLAQLEE 696
DB 1012 SGPRRTPGPTAEPLAGDRP-----TGHSSG-----RSPRRERRVPPARSESPR 1057
OY 697 ACR 699
DB 1058 ACR 1060

RESULT 9
US-08-748-483-1
; Sequence 1, Application US/08748483
; Patent No. 5955314
; -GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0157 US
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 57362
US-08-748-483-1

Query Match 3 6%; Score 159; DB 2; Length 181;
Best Local Similarity 29.1%; Pred. No. 1.6e-06;
Matches 39; Conservative 28; Mismatches 63; Indels 4; Gaps 3;

```

OY 68 RASPSPLTRMTKSLHSLLGDQDAVLPFTPLEREKCVDTLDFWPFACNGFROMNLKDTKT 127
DB 52 KTSIDEAL-QWRDSIDLKLLQNNYGLASFKSEFSENELEFWIACEDYKRIK-SPAKM 109
OY 128 LRVARAIYKRYIENNSVYSKOLKPAKTYIRDGIRKQOIGSVFDOAQTEIQAVMEENAY 187
DB 110 AEKAKQIIEEPIQTAPKRVENIDHFTKDTMKNLVPSLSS--FDMAQKRIHALMEKDSL 167
OY 188 OVFLTSIDILEYVR 201
DB 168 PRFVSEFYQELIK 181

```

```

RESULT 10
US-08-588-258B-32
; Sequence 32, Application US/08588258B
; Patent No. 5929207
; -GENERAL INFORMATION:
; APPLICANT: H. Robert Horvitz et al.
; TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,258B
; FILING DATE: January 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 01997/216001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-588-258B-32

```



```

: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/829,110
: FILING DATE: Filed Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0259 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 205 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: CLONE: 1216373
: US-08-829-110-6
:

```

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PE-0157 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4106
 TELEX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 205 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1216373
 US-08-748-483--5

RESULT 14
US-08-748-483-5
: Sequence 5, Application US/08748483
: Patent No. 5955314
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Goll, Surya K.
: TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: US
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/748,483
: FILING DATE: Herewith
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:

RESULT 15
 US-08-829-110-1
 : Sequence 1, Application US/08829110
 : Patent No. 5882890
 : GENERAL INFORMATION:
 : APPLICANT: Hillman, Jennifer L.
 : APPLICANT: Goli, Surya K.
 : TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
 : TITLE OF INVENTION: SIGNALING
 : NUMBER OF SEQUENCES: 6
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
 : STREET: 3174 Porter Drive
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94304
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/829,110
 : FILING DATE: Filed Herewith
 : CLASSIFICATION: 514
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Billings, Lucy J.
 : REGISTRATION NUMBER: 36,749
 : REFERENCE/DOCKET NUMBER: PF-0259 US
 : TELECOMMUNICATION INFORMATION:
 :

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2001, 10:57:16 ; Search time 25.04 Seconds
(without alignments)
2033.712 Million cell updates/sec

Title: US-09-587-574-1

Perfect score: 4445

Sequence: 1 MSSAVLVTLPLPPSSSFRED.....DETLPMEYGRILGKVERID 840

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*

6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*

7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*

8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*

9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*

10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*

11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*

12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*

13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*

14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*

15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*

16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*

17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*

18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*

19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*

20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*

21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*

22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4445	100.0	840	AAW93570	Human conductin pr
2	4445	100.0	840	AAW93569	Human conductin pr
3	1655	37.2	992	AAW96265	Murine axin. Homo
4	1605	36.1	900	AAW96264	Human axin. Homo
5	208	4.7	235	AAV97153	Human regulator of
6	193	4.3	235	AAV97154	Murine regulator o
7	172.5	3.9	220	AAW56929	Human prostate can
8	170.5	3.8	243	AAW30561	Human regulator of
9	168	3.8	181	AAW44834	Human p26 protein.
10	168	3.8	207	AAW54360	Human pancreatic c
11	167.5	3.8	116	AAV41020	RGS2 protein RGS r

12	166	3.7	196	22	AAW76863	Human lung tumour
13	166	3.7	217	20	AAW43847	Human cancer assoc
14	164.5	3.7	116	20	AAV41021	RGS3 protein RGS r
15	164	3.7	181	19	AAW44833	Rat p26 protein se
16	162.5	3.7	1182	20	AAV33496	Human SCA6 protein
17	161	3.6	115	20	AAV41019	RGS1 protein RGS r
18	161	3.6	181	19	AAW44835	Mouse p26 protein.
19	159	3.6	181	19	AAW62075	Human regulator of
20	159	3.6	181	21	AAV53931	A human regulator
21	156.5	3.5	118	20	AAV41001	Mouse RGS2 protein
22	153.5	3.5	1618	13	AAW27205	Human nestin. Hom
23	153	3.4	115	20	AAV41024	RGS10 protein RGS
24	152.5	3.4	118	20	AAV41000	Rat RGS4 protein R
25	152	3.4	159	19	AAW30560	Human regulator of
26	151.5	3.4	1618	15	AAW60127	Human nestin prote
27	151	3.4	2559	20	AAV41012	Amino acid sequenc
28	149	3.4	2510	16	AAW71007	Human neuronal cal
29	149	3.4	2510	16	AAW10579	Human calcium chan
30	146.5	3.3	116	20	AAV41022	RGS4 protein RGS r
31	146.5	3.3	202	17	AAW89895	p53 response prote
32	146.5	3.3	202	18	AAW08133	Human cytokine res
33	146.5	3.3	202	19	AAW59294	Human RATH1.1 prot
34	146.5	3.3	202	21	AAW87952	Human CRI protein.
35	146.5	3.3	570	18	AAW36002	Human Fchd531 gene
36	146.5	3.3	570	21	AAV45013	Protein encoded by
37	146	3.3	3266	21	AAW42491	Human ORFX ORF2255
38	144.5	3.3	2608	21	AAW85574	HS-UNC-53.3/GFP f
39	143.5	3.2	201	19	AAW58293	Mouse RATH1.1 prot
40	143	3.2	2385	21	AAW85569	Human homologue of
41	142.5	3.2	1187	16	AAW66451	AF-4 protein (enco
42	142.5	3.2	1210	16	AAW66450	AF-4 protein (enco
43	139.5	3.1	116	20	AAV41028	Human GAI protein
44	139.5	3.1	2091	21	AAW12000	Rat p3103 protein.
45	139	3.1	2432	21	AAW85565	Human homologue of

ALIGNMENTS

RESULT 1

ID AAW93570 standard; Protein: 840 AA.

XX AAW93570;

AC

XX

DT 17-JUN-1999 (first entry)

XX

DE Human conductin protein.

XX

KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;

KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;

KW Wntless signalling pathway; Adenomatous Polyposis Coll; APC;

KW tumour suppressor.

XX

OS Homo sapiens.

XX

PN W09911780-A2.

XX

PD 11-MAR-1999.

XX

PF 01-SEP-1998; 98WO-DE02621.

XX

PK -02-SEP-1997; 97DE-1038205.

XX

(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX

PI Behrens J, Birchmeier W;

XX

DR WPI. 1999-214706/18.

XX

DR N-PSDB; AAX23370.

XX

PT Tumor-suppressing protein conductin - used for treatment and

PT diagnosis of tumors

xx Claim 11; Fig 3; 22pp; German.

CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.

xx Sequence 840 AA;

Query Match 100.0%; Score 4445; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVLVTLPPSSSFRDAPRPVPEEGETPPCOPSVGVOSTKMPVSSNARNED 60
 DB 1 msaavlvtlppsssfredaprpvpgegetppcpqpsvkvqstklmpvssarnred 60
 QY 61 GIGEEGASPPSPITRWTKSLHSLGQDQAYLFRFLERKCVDTLDFWACNGFRQ 120
 DB 61 gigeegaspspltrwtkslshslgddqaylfrflerekcvtldfwacngfrqm 120
 QY 121 NLKDKTTLRVAKAIKRYIENNSVSKOLKPKATKYIRDGIRKQOIGSVMPDQOTEIO 180
 DB 121 nlkdktlrvakalkryiennsvskolkpkatkyirdgirkqoigsvmptdaqteio 180
 QY 181 VMEENAYVFLTSDIYLYEVNSGENTAYMSGIGSLKVLGVLPTLNEEWTCADLK 240
 DB 181 vmeenayvfltsdiylyevnsgentaymsgigslkvlgypltlneeewtcadlk 240
 QY 241 CKLSPTVVGSLSKTLRATASRSTETANGFRSPDPVHYVSGVYAPATSANDS 300
 DB 241 cklsptvvgslsktlratasrstetangfrspdpvhyvsgvyapatsands 300
 QY 301 ELSSDALTDSSMSMTDSSVDGVPYRMGSKOLOREHRSYKANGOVSLPHFPTHRLPK 360
 DB 301 elssdaldtdssmtsdssvdgvpymgskolorehrrsykangovslphfpthrlpk 360
 QY 361 EMTVEPAPFAELISRLKLEKLESHSLERLQOIREBEKGSQALSSRDGAPVQ 420
 DB 361 emtvepapaaelisrlklekleshslerlqoirebekgsqalssrdgapvq 420
 QY 421 HPALALPSGSYEEDPOTILDDLRLVLTQPCQSPGVGRYSPRSRSPDHNNHOOCH 480
 DB 421 hpalllpsgsyeedpqtildhlslrvlktpgcspgygrysprsrspdhnnhqqch 480
 QY 481 TLLSTGKLPVAAACPLLGKSFLLTKOTTKVHHNYIHHNAVPTKEIEAATQRYVCL 540
 DB 481 tllstgkllpvaacpllgksflltkottkvhhnyihhnavptkeieaatarvcl 540
 QY 541 CPGTDVYCYKSKSHKAPRLPGEOFGSGRTLPKRNAKGEPLGIALSARGGSSA 600
 DB 541 cpgtdvyckyckshkapeplpggefsgrtlpkrnakgeplgialsaraggsssa 600
 QY 601 AGGFOLPGEEDRSQDWOMWLESEKSKSPHSAQSIIRKSYPLESARAAGEVSRHHL 660
 DB 601 aggfqlpgeedrsdqdwomwleseksksphsaqsiirksyplesaraagevsrhhl 660
 QY 661 LGSAGHSRVARAHFPMQDAMPPLPNTLAQLEACRLAEVSKPOKORCCVASOORD 720
 DB 661 lgsaghsrvarahpfmqdamppltpntlaqleacrrlaevskpqkrcvsaasqrd 720
 QY 721 RNSAAGQAQASPPANSILAPEDHKEPKKLASVHALQASELVYTFEGCEIPIRRRLKA 780
 DB 721 rnsaagqaasppansilapedhkepkklasvhalqaselvytfegceiiprrmlka 780
 QY 781 QSLTLGHFKKQLSKKNRYRYFFKASDEFACGAFEEIMDETULPMYEEIRILGKVERID 840
 DB 781 qsltlghfkqlskknryryffkassdefacgafeeimdetulpmyeerilgkverid 840

DB 781 qsltlghfkqlskknryryffkassdefacgafeeimdetulpmyeerilgkverid 840

RESULT 2
 AAW93569
 ID AAW93569 standard; Protein: 840 AA.
 AC AAW93569;
 XX 17-JUN-1999 (first entry)
 DT Human conductin protein.
 DE
 KW Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour;
 KW therapy; cytoplasmic degradation; blockade; Wnt signalling pathway;
 KW wingless signalling pathway; Adenomatous Polyposis Coli; APC;
 KW tumour suppressor.
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Domain 78..200
 FT /note= "Regulator of G protein signalling domain as
 FT Binding-site 343..396 described in claim 12"
 FT /note= "GSK 3-beta binding region as described in
 FT Binding-site 397..465 claim 13"
 FT /note= "Beta-catenin binding domain as described in
 FT Region 783..833 claim 14"
 FT /note= "Dishevelled homology region as described in
 FT claim 15"
 PN MO9911780-A2.
 XX
 PD 11-MAR-1999.
 XX
 PF 01-SEP-1998; 98MO-DE02621.
 XX
 PR 02-SEP-1997; 97DE-1038205.
 XX
 PA (DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Behrens J, Birchmeier W;
 XX
 DR WPI: 1999-214706/18.
 DR N-PDB; AAX23369.
 XX
 PT Tumor-suppressing protein conductin - used for treatment and
 PT diagnosis of tumors
 PS
 PS Claim 11; Fig 1; 22pp; German.
 CC This invention describes a novel human conductin protein which has
 CC anti-tumour activity. Detecting the presence or amount of conductin,
 CC at protein or nucleic acid levels, is used to diagnose tumours, while
 CC agents that (re)activate conductin are used for tumour therapy.
 CC Conductin binds to beta-catenin and induces its cytoplasmic degradation,
 CC resulting in blockade of the Wnt/Wingless signalling pathway in
 CC vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
 CC fragments and, in conjunction with APC, acts as a tumour suppressor.
 XX
 SQ Sequence 840 AA;

Query Match 100.0%; Score 4445; DB 20; Length 840;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVLVTLPPSSSFRDAPRPVPEEGETPPCOPSVGVOSTKMPVSSNARNED 60
 DB 1 msaavlvtlppsssfredaprpvpgegetppcpqpsvkvqstklmpvssarnred 60

OY 61 GIGPEGRASPSPITRTWTKSLHSLGDDGAYLFRTELEEREKCVDTLDFMFACNGFROM 120
DB 61 g1gepegaspsdplrtckslhslgddgaylfrtleerekcvdtldfwaacngitqim 120
OY 121 NLKDKTTLVAKAIYKRYIENNSVSKOLKPATKTYIRDKIKKOOIGSMFDOAOETIOA 180
DB 121 nlkdkcttlvakaikyryiennsvskolkpatktyirdkikkgiigsmfdaqtelq 180
OY 181 VMEENAVOFLTSOYLEYEVNSGGENYAVMSNGGLSKVLGCGYPTLNEEEMTCADIK 240
DB 181 vmeenavofltsdyleyevnsggentaymsngglskvlcgypnlneeevctadik 240
OY 241 CKLSPTVVGSLSKTLRATASVSRSTETAEANGFRSRSDPVNPNHNGSCYVFAFATSANDS 300
DB 241 cklsptvvgslsktlratasvsrstetaeangfrsrdpvnphngscyvfaafatsands 300
OY 301 ELSSDALTDMSMTDSSVDGVPYRMGSKKOLQREMHRSYKANGQVSLPHFPRTHRLPK 360
DB 301 elssdaltdmsmtssvdgvpymgskkqlqremhrykangqvslphfprthrpk 360
OY 361 EMTPEPAFAAELISRLKLEKLEESRHSLEERLQOIREDEEKESQALSSRDGARVQ 420
DB 361 emtpepaafaellsrlekkleesrhsleerlqoiredeekesqalssrdgarvq 420
OY 421 HPLALPRSGSYEDRPQTLLDHLNLSVLKTRPGCQSPGVGRYSRSPRSRPHNNHNNHQQCH 480
DB 421 hplalprsgsyedrpqtlldhlnlsvlktrpgcspgvgrysrpsrphnnhnnhqqch 480
OY 481 TLLSTGGLPRPAACPLRLGSKSFLTKQTKNHNHNHNHNHNHNHNHNHNHNHNHNHNHN 540
DB 481 tllstggllprpaacplrlgsksflltkqtknhnhnhnhnhnhnhnhnhnhnhnhnhnhn 540
OY 481 tllstggllprpaacplrlgsksflltkqtknhnhnhnhnhnhnhnhnhnhnhnhnhnhn 540
OY 541 CPFGTDYVCYSKCKSHKPAERLPCEQFCGSRGGLPKRNKATGTERGLALSADGCMSSA 600
DB 541 cpfgtdyvcyskckshkpaerlpceqfcgsrgglprknaqtergjalalsardgcmssa 600
OY 601 AGCPOLPEEEDRODVMQWMLSESRQSKSPHSNOSTIRKSVPLRSARAPEREYSRHL 660
DB 601 agcpolpeeegrdovmqwmlseesrqsksphsnositrksvplrsarapereysrhl 660
OY 661 LGASGHSRVSARAHPTODPAMPPLTPNTLAOLEEACRRLAEVSKPOKORCVASQORD 720
DB 661 lgaaghsrvsarahptfdqamppltpnltlaqlleaecrilaevskprkqrcvasqord 720
OY 721 RNHSAGAGASPRANPSLAPEDHKEPKKLASVALQASELVVTFPCGEEIPIYRMILKA 780
DB 721 rnhsaagagaspranpslapedhkepkklasvalqaselvvtyffcgeeipiyrmilka 780
OY 781 OSLTIGHNRKEOLSKGNRYVFKKASDFACGAVFEETIMDDETVLPMEGRITLGVERTD 840
DB 781 osltighnrkeolskgnryvfkksdfacgavfeetlmdetvlpmyegritlgvertd 840

RESULT 3
ID AAM96265 standard: Protein: 992 AA.

XX AAM96265;
XX 14-JUN-1999 (first entry)
XX Murline axlin.
XX Axlin; cancer; breast cancer; colorectal cancer;
KW gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
KW diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
KW beta-catenin.
XX Mus musculus.
XX MO9902179-A1.
XX

PD 21-JAN-1999.
XX 09-JUL-1998; 98WO-US14414.
XX 10-JUL-1997; 97US-0890865.
XX (UYCO) UNIV COLUMBIA NEW YORK.
PI Constantini F, Zeng L;
XX WPI: 1999-120510/10.
DR N-PSDB; AAX09013.
XX
PT Newly isolated nucleic acid encoding "axis inhibition" protein
PI (Axin) - useful for detecting, diagnosing and treating cancer
XX
PS Claim 8; Figure 8; 95pp; English.
CC Nucleic acids encoding mutant and wild type Axin and
CC oligonucleotides derived from them are useful for detecting
CC mutations in the Axin gene and for determining whether a subject is
CC likely to develop cancer (including breast, colorectal,
CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axin and homologues of Axin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.
XX
SQ Sequence 992 AA:

Query Match 37.2%; Score 1655; DB 20; Length 992;
Best Local Similarity 42.7%; Pred. No.2.4e-128;
Matches 390; Conservative 133; Mismatches 246; Indels 144; Gaps 30;

OY 12 DSSSFREDAPRPYPGEERGE-----TPPCQPSV--GKVQSTKPMFVSSNARNEDGLG- 63
DB 12 dsssfredaprpypgeegelvsidsrvmhsfcsqkgtlsksetatprsdldlgy 199
OY 64 EPEGASPSPLRTWTKSLHSLGDDGAYLFRTELEEREKCVDTLDFMFACNGFROMNLK 123
DB 64 epegaspsplrtwtkslhslgddgaylfrtleerekcvdtldfwaacngitqim 123
OY 200 epegaspsplrtwtkslhslgddgaylfrtleerekcvdtldfwaacngitqim 259
DB 200 epegaspsplrtwtkslhslgddgaylfrtleerekcvdtldfwaacngitqim 259
OY 124 DT---KTLVAKAIYKRYI-ENNSVSKOLKPATKTYIRDKIKKOOIGSMFDOAOETIO 179
DB 124 dt---ktlvakaikyryi-ennsvskolkpatktyirdkikkgiigsmfdaqtelq 179
OY 260 dsnееkrklaratayrkyllidngivsrqtkpatksfkldecvmkqdlpamfdqatqlq 319
DB 260 dsnееkrklaratayrkyllidngivsrqtkpatksfkldecvmkqdlpamfdqatqlq 319
OY 180 AVMEENAVOFLTSOYLEYEVNSGGENYAVMSNGGLSKVLGCGYPTLNEEEMTCADIK 236
DB 180 avmeenavofltsdyleyevnsggentaymsngglskvlcgypnlneeevctadik 236
OY 320 stmeentypsfllksdyleytrtgsesprkvcsgsgstgymagylptlneedeewkcd 379
DB 320 stmeentypsfllksdyleytrtgsesprkvcsgsgstgymagylptlneedeewkcd 379
OY 237 -----ADLKCKLSPTVVGSLSKTL-----RATASVSRSTETAEANGFRSRSDPVNPNH 285
DB 237 -----adlkcklsptvvgslsktl-----ratasvsrstetaeangfrsrdpvnph 285
OY 380 qdadddgdrpdlrps--rltqlkllletaaprsstrynegreltygswr--evnpyuv 435
DB 380 qdadddgdrpdlrps--rltqlkllletaaprsstrynegreltygswr--evnpyuv 435
OY 286 GSGYVFAFATSANDSE---LSSDALTDMSMTDSSVDGVPYRMGSKKOLQREMHRSYK 342
DB 286 gsgyvfaafatsandse---lssdaltdmsmtssvdgvpymgskkqlqremhrykangqv 342
OY 436 nsqyalapatsandeeqglsdda---dlstltdssvdgippyrl--rqhntremesig 490
DB 436 nsqyalapatsandeeqglsdda---dlstltdssvdgippyrl--rqhntremesig 490
OY 343 ANGQVSLPHFPTTHRLPKEMTPVERPAFAAELISRLKLEKLEESRHSLEERLQOIREDE 402
DB 343 angovslphfptthrlpkemtpverpaafaaelisrllekkleesrhsleerlqoirede 402
OY 491 vngvrplrpipritympkeir--vepqkfaeelhlrlaevgrtreaeekleerlkrymee 549
DB 491 vngvrplrpipritympkeir--vepqkfaeelhlrlaevgrtreaeekleerlkrymee 549
OY 403 EKEGSRQALSSRDGARVQVGRPLALLPS-----GSEEDRPQTLLDHLNLS 445
DB 403 ekegsrqalssrdgarvqvgvgrplallps-----gseedrpqtlldhlnls 445
OY 550 egedgemp-----sgpmashklsrvaawhlfprpyvdmgsgjlrdaeenpeslldehvr 605
DB 550 egedgemp-----sgpmashklsrvaawhlfprpyvdmgsgjlrdaeenpeslldehvr 605
OY 446 VLKTPCQSPGVGRYSRSPRSRPHNNHNNHQQCHTLLSTGGLPRPAACPLRLG- 500

```

Db 606 ymrtpcgspg-----pghrpsdsg-----vaktavlggtasgh 640
QY 501 -----KSFLEKQTT-----KHVHHYIHHNAVKTKEIEAATQRYVCLCGGIDYCY 550
Db 641 gkhvpxlglkldtaglhhhrvhh-vhhnsa-trkeqmaevavrtvsgsfwsgpeltgh 698
QY 551 SKCSKHPK-APRPL-PGEQFCGSRGGTLPRKNAGTEPGLALSARDGMSAAGPOLPG 608
Db 699 akprysenagtltsagdlpfvgktsapskrnlkkaesgkana-----evps 746
QY 609 --EEGDRSODVWQWMLSEERO---SKSKPHSQSIRKSYPLESAAACGERVSRHLLICA 663
Db 747 ltedaeknqkimgwlllegekeisrthkaghsaglrkqahessrplsiervgavhpwvs 806
QY 664 SGHSRVARHPFTQDPAMPPLTPPTLAOLEACRRLAEVSK-----POKORCCVASQ 718
Db 807 aqlrsvpsnlflgdpmpnpapnpltlglearrileeekranklpskqrvyqavmq 866
QY 719 RDRHNSAAGAGASFPANP-----SLAPEDHKEPKKLASVHALQASELVVYTF 767
Db 867 r-----grtcvrcpacarvlsvpavsdlelseteksgtkaggsapcdslvgyyf 919
QY 768 CGEIPRYRMKKAOSLTIGHFKESQSKGNRYVEKKASDEFACGAVPEELTMDFTVLP 827
Db 920 cgepiptyltvgravlglgkelltkkgsyrytkvdsdfcgvfveevredapvlrv 979
QY 828 YEGRIKVERID 840
Db 980 feekligkevkd 992

```

RESULT 4

AAW96264 standard; Protein: 900 AA.

AAW96264;

14-JUN-1999 (first entry)

Human axin.

Axin: Cancer: breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
beta-catenin.

Homo sapiens.

MO9902179-A1.

21-JAN-1999.

09-JUL-1998; 98MO-US14414.

10-JUL-1997; 97US-0890865.

(UYCO) UNIV COLUMBIA NEW YORK.

Constantin F, zeng L,

WPI, 1999-120510/10.

N-PSDB; AAX09012.

Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer

Disclosure: Figure 11, 95pp; English.

Nucleic acids encoding mutant and wild type Axin and
oligonucleotides derived from them are useful for detecting
mutations in the Axin gene and for determining whether a subject is
likely to develop cancer (including breast, colorectal,

CC gastrointestinal, esophageal, carcinomas or melanomas). The wild
CC type Axin and homologues of Axin are useful for treating subjects
CC who are likely to develop cancer (thyroid carcinomas). The nucleic
CC acids are also useful for diagnosing cancer and for detecting
CC mutations in cancerous cells. Wild type Axin, its antisense
CC molecule and identified compounds form pharmaceutical compositions
CC in the treatment of cancer. The compositions are also useful for
CC treating cancer by inhibiting tumorigenesis (by inducing degradation
CC of beta-catenin). The nucleic acid encoding Axin acts through
CC negative regulation of the Wnt pathway in the Nieuwkoop Center.

Sequence 900 AA;

Query Match 36.1%; Score 1605; DB 20; Length 900;

Best Local Similarity 41.2%; Pred. No. 2.9e-124;

Matches 382; Conservative 123; Mismatches 248; Indels 172; Gaps 29;

```

QY 12 DPSSFRDAPRPVPEEGETPPCOPSVGKQSTKMPVS-----SN 54
Db 48 dlgsafedaprpvpege-----lvstprpsysfcskgyglketstat 97
QY 55 ARNEDGIG-EPGRASPSPLTRWTSLSHSLGDQCAVLFRTLEKCVDTDFWEA 113
Db 98 prrsdllyepesgsasrtppylkwaeslnsllddggisifrtflkxgcadlldfwa 157
QY 114 CNGFROMMLKDT--KTLRVAKAIYKRYI-ENNSVSKOLKPAKTIYRGIKKQOQGSV 169
Db 158 ctgfrklrpecdsneekrlklaralyrykylldnglvarqtkpacksfkcmqldpa 217
QY 170 MFDQATEIOAVMENAYOVFLSDIYLEYVSGGENTAVMS--NGLAGSLKVLGQIPT 227
Db 218 mfdagteiqatmeentylpsflkedilyeyltrtgsesprkcsdsgsgykgklsylypt 277
QY 228 LNEEEMTC-----ADLKCKSPYVVGSLSTLATASVRSFTEAENCFRFR 276
Db 278 lneeeewkcdqdmddgrdaapgrl-pqkliletaaprsvsrrysgretfyswr 335
QY 277 SDPVPYHVGSGYVFAPATSANDE--LSSDALTDMSMTQSVGVPPYRMGSKOL 333
Db 336 -epnpyynagyalapataandegsjsda---dlsltdsvdglppryl--tkqh 389
QY 334 QREKHSVKANGOVSLPHFRTHRLPREMTVEPARAFAELSLREKLLELSRHSLE 393
Db 390 rremgesayngyvrphlprtylvkrv-vepqkfaeelhrlaeavgtreaeeeklee 448
QY 394 RLOQIREDEKEGSEQLSSRDGAPV--HPLALLS-----G 429
Db 449 rlxrvmeege-----dgdpsgpprpbcklprapawhfprrlctwacaglld 499
QY 430 SYEDPQTLDDHLRYLKTGGCQSPGVGRYSPRSRSPDHNNHNOCHTLSTSGKL 489
Db 500 aheepeslidenhgyrlrtgrgsps-----pghrpsdsgv-----akm 540
QY 490 PVAACPLLGKSFLEKQTT-----HVHHYIHHNAVKTKEIEAATQRYV 539
Db 541 pvalggaasgghkhpksaklaaglhhrvhhv--hstsrarkeqveaattraqs 598
QY 540 LCPGCTDIYCYSK-----CSHKAPEPLPGEQFCGSRGGTLPRKNAGTEPGLASARD 594
Db 599 sfawglepshgarsrgysesvgaapnasgdlahsg-kyvackrlnakkaesgsast 655
QY 595 GGMSSAAGPOLPG--EEGDRSODVWQWMLSEERO---SKSKPHSQSIRKSYPLESARA 649
Db 656 -----evrgaadeaknqkimgwlllegekeisrthrtgngsgtrkqpghenstr 705
QY 650 APGERVSRHHLGASGHSRVARHPFTQDPAMPPLTPPTLAOLEACRRLAEVSK 706
Db 706 -----lslhpwagpqlrtsvpsnlflgdpmpnpapnpltlglearrileeekrs 760
QY 707 --POKORCCVASQORBRNSAAGAGASFPANP-----SLAPEDHKEPKKLAV 753
Db 761 rapskgrvygevmt-----gracvrcpacarvlhvpavsdmelelsetrtsgtkvgyg 813

```


AC AAY97154;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 DE Murine regulator of G-protein signaling protein.
 XX
 XX RGS; regulators of G-protein signaling; GTPase activating protein; GAP;
 KW G-alpha protein; cell adhesion; chemotaxis; vulnerability; immunosuppressor;
 KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
 KW cytoskeletal; hepatotropic; anti-anaemic; modulator; gene therapy.
 XX
 OS Mus sp.
 XX
 XX Key
 FH Domain
 FT Location/Qualifiers
 FT 82..201
 FT /label= RGS_domain
 FT Misc-difference 83 /note= "forms part of hydrophobic core"
 FT Misc-difference 90 /note= "forms part of hydrophobic core"
 FT Misc-difference 100 /note= "forms part of hydrophobic core"
 FT Misc-difference 103 /note= "forms part of hydrophobic core"
 FT Misc-difference 104 /note= "forms part of hydrophobic core"
 FT Misc-difference 107 /note= "forms part of hydrophobic core"
 FT Misc-difference 109 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 111 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 112 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 115 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 116 /note= "forms part of hydrophobic core"
 FT Misc-difference 138 /note= "forms part of hydrophobic core"
 FT Misc-difference 139 /note= "forms part of hydrophobic core"
 FT Misc-difference 142 /note= "forms part of hydrophobic core"
 FT Misc-difference 143 /note= "forms part of hydrophobic core"
 FT Misc-difference 151 /note= "forms part of hydrophobic core"
 FT Misc-difference 152 /note= "forms part of hydrophobic core"
 FT Misc-difference 154 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 183 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 184 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 187 /note= "forms part of hydrophobic core"
 FT Misc-difference 188 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 189 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 191 /note= "forms part of hydrophobic core"
 FT Misc-difference 192 /note= "Makes direct contact with G-alpha-1"
 FT Misc-difference 193 /note= "forms part of hydrophobic core"
 FT Misc-difference 198 /note= "forms part of hydrophobic core"
 FT Misc-difference 198 /note= "forms part of hydrophobic core"
 XX
 XX WO200046236-A2.
 XX

PD 10-AUG-2000.
 XX
 XX
 PF 04-FEB-2000; 2000WO-US02977.
 XX
 PR 04-FEB-1999; 99US-0244314.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Hodge MR, Yowe D;
 XX
 DR WPI: 2000-532893/48.
 DR N-PSDB; AAA52090.
 XX
 PT Novel regulator of G-protein signaling nucleic acids and polypeptides,
 PT useful as diagnostic and investigative tools and to treat G-protein
 PT signaling disorders
 XX
 PS Claim 8; Page 104; 105pp; English.
 XX
 CC The RGS (regulators of G-protein signaling) protein genes, clones
 CC AAH16395 and m1975, were identified in human and murine spleen cDNA
 CC libraries, respectively. Both proteins have unique N- and C-terminal
 CC sequences. The C-terminal location of the RGS domain is consistent with
 CC RGSs known to act as GTPase activating proteins (GAPs) for G-alpha
 CC proteins. G-alpha-1 linked receptors support rapid adhesion and directed
 CC migration of leukocytes and other cell types. The novel RGS proteins may
 CC be used to modulate cell adhesion and chemotaxis, e.g. for aiding wound
 CC repair. The RGS proteins, related cDNAs and anti-RGS antibodies are
 CC useful for modulation, diagnosis and treatment of immune and respiratory
 CC disorders.
 XX
 SQ Sequence 235 AA;
 XX
 Query Match 4.3%; Score 193; DB 21; Length 235;
 Best Local Similarity 28.1%; Pred. No. 6,7e-08;
 Matches 50; Conservative 37; Mismatches 69; Indels 22; Gaps 5;
 QY 41 GKVSSTKPMPPVSNARRE-----DGLGE-----PGRASPSDPLRWTKSL 82
 DB 29 gkeetsleakirakekennrlslilqprdfngetqasrallaketrvspearv kwesf 87
 QY 83 HSLGDGDGAYLFRFLEREKCVDTLDFEACNGFRQNLKDTLRVAKAIYRYENN 142
 DB 88 dklshrdgvdafrflkftfseenielfwacedfkck-epqqlilkakayekfiqnd 146
 QY 143 SVSKQLKPAKTYIRSGIKRQKQIGSVWFDAQRIEIQAVMEENAYOVLTSDILEVY 200
 DB 147 apkevnldfnkeviakslagptlsh--fdtagarvyvymehdsyxtlksetylhll 202
 XX
 RESULT 7
 ID AAB56929 standard; Protein: 220 AA.
 AC AAB56929;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen protein sequence SPO ID NO:1507.
 XX
 XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytoskeletal; cardiovascular; immunomodulatory; muscular;
 KW vulnerability; gastrointestinal; nephrotropic; anti-infective; gynecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200055174-A1.
 PN
 XX
 PD 21-SEP-2000.
 XX


```

PF 08-MAR-2000; 2000WO-US05988.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
DR WP1: 2000-587513/55.
XX N-PSDB: AAF16132.
PT
PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -
XX
PS Claim 11: Page 1946-1947; 238np; English.
XX
CC AAF15566 to AAF16505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytosolic,
CC cardiactive, immunomodulatory, muscular, vulnary, gastrointestinal,
CC neohrotropic, antinefctive, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 220 AA;
XX
Query Match 3.9%; Score 172.5; DB 21; Length 220;
Best Local Similarity 26.9%; Pred. No. 3,1e-06;
Matches 46; Conservative 24; Mismatches 72; Indels 29; Gaps 4
QY 30 EGEPPPCOPSVCKVQS---TKPMVSSNARNNEGLGEPGRASPDSPLTRMTKSLSL 85
DB 59 qnssepqkpkcgkkskqgqfllkpspeaal-----wseafdel 96
QY 86 LGDDQDAALFRFRLERKCVDTLDFWFAFCNGEFGOMNLKDTKTLRAKAIKRYIENNSVY 145
DB 97 laskyglaafrflsefeenlefwlacedfkktc-spqklsksarkklytdfiekcapk 155
QY 146 SKQKLPATKTYTRDGIKIKKQOIGSVWPDQAQETIQAVMEENAVQVRLTSDTY 196
DB 156 einldfgklllaqnl--qeatsgfttaqkrivyslimensyprflseefy 204
RESULT 8
AAW30561
ID AAW30561 standard; Protein: 243 AA.
XX
XX AAW30561;
AC
XX
DT 18-JAN-1999 (first entry)
XX
DE Human regulator of G-protein signalling 2 (RGPS-2).
XX
KW Regulator of G-protein signalling 2; RGPS-2; human;
KW G protein coupled receptor; signal transduction; inflammation;
KW cell proliferation; cancer; diagnosis; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX 126..142
XX Region /note="potential G-protein coupled receptor

```

FT		signature"
FT	Region	58..177
FT	/note=	"RGF motif"
FT	Modified-site	8..11
FT	/note=	"Asn may be N-glycosylated"
FT	Modified-site	235..238
FT	/note=	"potential cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT	Modified-site	11..14
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Modified-site	66..69
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Modified-site	220..223
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Modified-site	93..95
FT	/note=	"potential protein kinase C phosphorylation site"
FT	Modified-site	97..99
FT	/note=	"potential protein kinase C phosphorylation site"
FT	Modified-site	161..164
FT	/note=	"potential protein kinase C phosphorylation site"
XX	M09844115-A2.	
XX	PD	08-OCT-1998.
XX	PR	31-MAR-1998;
XX	PR	98WO-US06336.
XX	PA	31-MAR-1997;
XX	(INCYTE)	INCYTE PHARM INC.
XX	Goli SK,	Hillman JL:
XX	WP1;	1998-557112/47.
DR	N-PSDB;	AAV45442.
XX	PT	New regulators of G-protein signalling - useful for, e.g. diagnosis, prevention and treatment of cancer and inflammation
XX	PS	Claim 19; Page 45; 65pp: English.
XX	CC	This is the amino acid sequence of a novel human regulator of G-protein signalling, termed RGPS-2. It was deduced from a consensus nucleic acid sequence (see AAV45442) derived from thymus and other CDNA clones. RGPS-2 shares 46% and 37% identity with human BL34 and RGS4, respectively. It shows significant expression in inflamed, immortalised or cancerous cells and tissues. The invention provides 2 regulators of G-protein signalling, i.e. RGPS-2 and RGPS-1 (see AAW30560). The invention also features nucleic acids encoding RGPS polypeptides, oligonucleotides, peptide nucleic acids, fragments, portions or antisense molecules, and expression vectors and host cells. It also features antibodies specific for RGPS, and pharmaceutical compositions comprising purified RGPS. It also provides methods for stimulating cell proliferation using an RGPS or an agonist of CC RGPS and for treating or preventing disorders (e.g. cancer) associated with cell proliferation and inflammation using an antagonist of RGPS.
SO	Sequence	243 AA:
Query Match	3.8%; Score 170.5; DB 19; Length 243;	
Best Local Similarity	28.1%; Pred. No. 5.2e+06;	
Matches	55; Conservative 38; Mismatches 78; Indels 25; Gaps	
14	SSSFREDAPRPYPGESEGTTPCQPSVKGVOSTKPMPVSSNARNRNDGLGEPEGGRASP-	72
7		

[illegible]

Db 128 qk1qg4lfnlmkydsysrflkxsdflfkxkrtree 161

RESULT 10
AAB54360
ID AAB54360 standard; Protein; 207 AA.
XX
AC AAB54360;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:812.
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW detection; diagnosis; identification; cytostatic; neuroprotective;
KW neoplastic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW antineoplastic; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic;
KW neural; immune system; muscular; reproductive; gastrointestinal;
KW pulmonary; cardiovascular; renal; proliferative.
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05989.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-579444/54.
XX
DR N-PSDB: AAC99125.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
XX
XX
XX Claim 11; Page 1267-1268; 1379pp; English.
XX
XX
XX AOC98773 to AAC99231 encode the human pancreatic cancer associated
XX proteins, called pancreatic cancer antigens, given in AAB54408 to
XX AAB54406. The human pancreatic cancer antigens have cytostatic,
XX neuroprotective, neoplastic, immunomodulatory, relaxant, contraceptive,
XX gynaecological, cardiant and antineoplastic activities, and can be used
XX in gene therapy. The polynucleotide and proteins can be used for
XX preventing, treating, or ameliorating a medical condition or in assays
XX for diagnosing a pathological condition or a susceptibility to one in a
XX subject. Binding partners to the proteins and the activity of the
XX proteins can be identified. The pancreatic cancer antigens can be used to
XX detect, treat or prevent pancreatic disorders, especially cancer.
XX Agonists and antagonists to the antigens can be screened for. The
XX pancreatic cancer antigen polynucleotides can be used to design nucleic
XX acid hybridisation probes that can be used in chromosome mapping, linkage
XX analysis, tissue identification and/or typing and a variety of forensic
XX and diagnostic methods. The proteins can be used to generate antibodies
XX which are used to vitro, detect and target the polypeptides, including
XX both in vivo and in vitro diagnostic and therapeutic methods. The
XX proteins can be used to treat or prevent neural, immune system, muscular,
XX reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
XX proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
XX sequences used in the exemplification of the present invention.
XX
XX Sequence 207 AA;

Query Match 3.8%; Score 168; DB 21; Length 207;
Best Local Similarity 28.6%; Pred.No. 6.6e-06;

Matches 44: Conservative 37; Mismatches 65; Indels 8; Gaps 4;

OY 56 RRNEGCLCEPGRASP-----SPLTRWTKSLHSLGGDGAFLPRTFLEREKCVDTLDFW 111
 Db 38 krpssdldssgssssshqslstakwaaslenlledpegvkrfrfllkkesenwltw 97

OY 112 FACNGFROMNKKDKTTLVAKAIYKRYIENNSVSKQLKPTKTYIRGIRKQOIGSVWF 171
 Db 98 lacedfkmgdk-qimgqakelymtfl--sskassqynvqgsarlneklleep-hplmf 153

OY 172 DOAOTEIOAVMEENAYOVFLTSDIYLEXVRSQGE 205
 Db 154 qkldqqlfmlmkysdysrflksdflfkhkrtee 187

RESULT 11
 AAY41020
 ID AAY41020 standard; protein: 116 AA.
 AC AAY41020:
 XX
 DT 06-DEC-1999 (first entry)
 XX
 DE RGS2 protein RGS region.
 XX
 KM RGS: guanine nucleotide exchange factor; GEF: RGS domain; GAS: cancer;
 KM G protein alpha subunit; cell proliferation; growth control; hemostasis;
 KM morphogenesis; stress fiber formation; integrin-mediated interaction;
 KM embryonic development; tumor cell growth; cell death; leukocyte homing;
 KM bone resorption; clot retraction; db1 homology domain; mechanical stress;
 XX pleckstrin homology domain.
 XX
 OS Unidentified.
 XX
 PN WO3947557-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-US06051.
 XX
 PR 18-MAR-1998; 98US-0078634.
 XX
 PA (ONYX-) ONYX PHARM INC.
 XX
 PI Bollag G, Hart MJ, Roscoe W, Polakis P, Sternweis P, Kozasa T;
 PI Jlang X;
 XX
 DR WPI: 1999-571821/48.
 XX
 PT New isolated RGS-GEF polypeptides, used to develop products for
 PT modulating, e.g. cell proliferation and integrin-mediated interactions
 PT
 PS Disclosure: Fig 18; 75pp; English.
 PS
 XX The invention relates to isolated RGS-guanine nucleotide exchange factor
 CC (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of
 CC an RGS domain of a GEF protein and does not comprise a db1 homology (DH)
 CC domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides
 CC can be used for modulating an activity of a G protein alpha subunit
 CC (GAS). The products can be used for the regulation of biological pathways
 CC in which a RGS-GEF polypeptide is involved, particularly pathological
 CC conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth
 CC control, stress fiber formation, and integrin-mediated interactions,
 CC such as embryonic development, tumor cell growth and metastasis,
 CC programmed cell death, hemostasis, leukocyte homing and activation, bone
 CC resorption, clot retraction, and the response of cells to mechanical
 CC stress. The products can also be used for detection, diagnosis and
 CC production of transgenic animals. Sequences AAY41014-028 represent RGS
 CC regions of several proteins.
 CC
 XX Sequence 116 AA;

Query Match 3.8%; Score 167.5; DB 20; Length 116;
 Best Local Similarity 32.8%; Pred. No. 3e-06; Mismatches 3; Gaps 2;
 Matches 39; Conservative 20; Mismatches 57; Indels 3;

OY 78 WTKSLHSLGGDGAFLPRTFLEREKCVDTLDFWFCNGFROMNKKDKTTLVAKAIYKR 137
 Db 1 wseatdelaaakygaiaetralfksecenlefwaicedfkktk-spqklsskarxlytd 59

OY 138 YIENNSVSKQLKPTKTYIRGIRKQOIGSVFDOAOTEIOAVMEENAYOVFLTSDIY 196
 Db 60 ftekeaprelnldfgtklliaqnl--geatsgcftaqkryslmenssypflseesfy 116

RESULT 12
 AAB76863
 ID AAB76863 standard; protein: 196 AA.
 AC AAB76863:
 XX
 DT 12-APR-2001 (first entry)
 XX
 DE Human lung tumour protein related protein sequence SEQ ID NO:339.
 XX
 KM Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
 KM lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
 KM cyrostatic; antisense inhibition.
 XX
 OS Homo sapiens.
 XX
 PN WO200100828-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US18061.
 XX
 PR 30-JUN-1999; 99US-0346492.
 PR 15-OCT-1999; 99US-0419356.
 PR 17-DEC-1999; 99US-0466867.
 PR 30-DEC-1999; 99US-0476300.
 PR 06-MAR-2000; 2000US-0519642.
 PR 22-MAR-2000; 2000US-0533077.
 PR 10-APR-2000; 2000US-0546259.
 PR 27-APR-2000; 2000US-0560406.
 PR 05-JUN-2000; 2000US-0589184.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
 PI Retter MW, Mannion J;
 XX
 DR WPI: 2001-071488/08.
 XX
 PT Lung tumor-associated proteins and the nucleic acids that encode them,
 PT useful for preventing, diagnosing and treating lung cancer -
 PT
 PS Example 1; Page 271-272; 436pp; English.
 PS
 XX The present invention describes immunogenic portions of lung tumour-
 CC associated proteins (I) and the nucleic acids (NAs) that encode them.
 CC (I) have cytostatic activity and can be used in gene therapy, antisense
 CC inhibition and in vaccines. The NAs and the lung tumour-associated
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with their inappropriate expression,
 CC especially lung cancers. For example, the NAs may be administered to
 CC treat diseases by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of the protein by expressing inactive proteins
 CC or to supplement the patient's own production of (I). Additionally, the
 CC NAs may be used to produce the lung-tumour associated protein, according
 CC to standard recombinant-DNA methodology. Conversely, antisense NA
 CC molecules may be administered to down regulate protein expression by
 CC binding with the cells own genes and preventing their expression. The NA
 CC and complementary sequences may also be used as DNA probes in diagnostic

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2001, 11:01:57 ; Search time 14.92 Seconds

(Without alignments)
1928.593 Million cell updates/sec

Title: US-09-587-574-1

Perfect score: 4445
1 MSSAVLVTLDPDPSSFRD.....DETULPMYEGRIKVERID 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SWISSPROT_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4445	100.0	840	1 AXN2-MOUSE	088566 mus musculu
2	4310	97.0	838	1 AXN2-RAT	070240 ratius norv
3	4027.5	90.6	843	1 AXN2-HUMAN	Q9Y2L1 homo sapien
4	2632.5	59.2	812	1 AXN2-BRARE	P57095 brachydanio
5	1736	39.1	841	1 AXN-CHICK	042400 gallus gall
6	1661	37.4	893	1 AXN1-RAT	070239 ratius norv
7	1655	37.2	992	1 AXN1-MOUSE	035625 mus musculu
8	1654.5	37.2	842	1 AXN1-XENLA	Q9Y9Y0 xenopus lae
9	1628	36.6	835	1 AXN1-BRARE	P57094 brachydanio
10	1605	36.1	900	1 AXN1-HUMAN	015169 homo sapien
11	457.5	10.3	745	1 AXN1-DROME	09V407 dtrosophila
12	195	4.4	547	1 RGSE-MOUSE	P97492 mus musculu
13	190.5	4.3	544	1 RGSE-RAT	008773 ratius norv
14	189.5	4.3	519	1 RGSE-HUMAN	P49796 homo sapien
15	172.5	3.9	211	1 RGSE2-HUMAN	P41220 homo sapien
16	170.5	3.8	211	1 RGSE2-MOUSE	008849 mus musculu
17	167	3.8	167	1 RGSA-HUMAN	043665 homo sapien
18	164	3.7	180	1 RGSE-HUMAN	P57771 homo sapien
19	163	3.7	180	1 RGSE-RAT	P49804 ratius norv
20	161.5	3.6	216	1 GAIP-RAT	070521 ratius norv
21	159	3.6	181	1 RGSS-HUMAN	015539 homo sapien
22	159	3.6	196	1 RGSL-HUMAN	008116 homo sapien
23	157.5	3.5	205	1 RGSD-HUMAN	P49798 homo sapien
24	156.5	3.5	217	1 GAIP-HUMAN	P49795 homo sapien
25	154.5	3.5	181	1 RGSS-MOUSE	008850 mus musculu
26	154.5	3.5	205	1 RGSD-RAT	P49799 ratius norv
27	153	3.4	202	1 RGSG-BOVIN	046471 bos taurus
28	151.5	3.4	199	1 RGSG-RAT	P56700 ratius norv
29	151.5	3.4	205	1 RGSA-MOUSE	008899 mus musculu
30	151.5	3.4	1618	1 NEST-HUMAN	P48681 homo sapien
31	150.5	3.4	181	1 RGSS-RAT	P49800 ratius norv
32	149	3.4	159	1 RGSD-HUMAN	014921 homo sapien
33	149	3.4	2505	1 CCAA-HUMAN	000555 homo sapien

ALIGNMENTS

RESULT ID	AXN2-MOUSE	STANDARD	PRT	840 AA.
AC	088566: 090X16:			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)			
DE	(AXIL).			
GN	AXIN2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96221239; PubMed=9554852;			
RA	Behrens J., Jerchow B.A., Wuerle M., Grimm J., Asbrand C.,			
RA	Wirtz R., Kuehl M., Wedlich D., Birchmeier W.;			
RT	"Functional interaction of an axin homolog, conductin, with beta-			
RT	catenin, APC, and GSK3beta."			
RL	Science 280:596-599(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,			
RA	Jenkins N.A., Warburton D., Constantini F.;			
RT	"Properties of mouse Axin2 and human AXIN2: chromosomal location,			
RT	expression pattern, interaction with Axin and effects on embryonic			
RT	axis formation."			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES			
CC	BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-			
CC	CATENIN AND APC BY GSK-3B (BY SIMILARITY).			
CC	- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)			
CC	AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN			
CC	OCCURS VIA THE ARMD/ILDO REPEATS CONTAINED IN BETA-CATENIN.			
CC	TERMINAL COMPLEX (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).			
CC	- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY			
CC	PP2A (BY SIMILARITY).			
CC	- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	- SIMILARITY: CONTAINS 1 DIX DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AF073788; AAC6047.1; -			095208 ovis aries
DR	EMBL; AF205889; AAF22800.1; -			015492 homo sapien
DR	MGI; MGI:1270862; Axin2.			P97428 mus musculu
DR	HSSP; P49799; IAGR.			P51823 homo sapien
DR	InterPro; IPR000342; -			014924 homo sapien
				Q9Y263 homo sapien
				Q18312 caenorhabdi
				P79348 bos taurus
				P29617 dtrosophila
				P46821 homo sapien
				Q14687 homo sapien
				Q03172 mus musculu

DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR PROSITE: PS50132; RGS; 1.
 KW Anti-oncogene: Phosphorylation.
 FT DOMAIN 81 200 RGS.
 FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY SIMILARITY).
 FT DOMAIN 469 476 DIX.
 FT DOMAIN 758 840 POLY-HIS.
 FT CONFLICT 101 101 R -> K (IN REF. 2).
 FT CONFLICT 474 474 H -> Y (IN REF. 2).
 FT CONFLICT 484 503 S -> P (IN REF. 2).
 FT CONFLICT 503 503 F -> S (IN REF. 2).
 FT CONFLICT 603 603 G -> A (IN REF. 2).
 SQ SEQUENCE 840 AA: 92934 MW: A07D5BF825DE7277 CRC64;

Query Match 100.0%; Score 4445; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred. No. 9.9e-244;
 Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVLVTLDPSSSFREDAPRPVGEETPPCOPSVGVSTKPMVSNARNED 60
 DB 1 MSSAVLVTLDPSSSFREDAPRPVGEETPPCOPSVGVSTKPMVSNARNED 60
 QY 61 GLGPEGRASPDSPLTWTKSLHSLDGDQAVLFRFLEREKCVDTLDFEACNGFROM 120
 DB 61 GLGPEGRASPDSPLTWTKSLHSLDGDQAVLFRFLEREKCVDTLDFEACNGFROM 120
 QY 121 NLKTKTLRAKAIYKRIENNSVSKQKPAFTYTRDGIKQOIGSVWFDAQTEIOA 180
 DB 121 NLKTKTLRAKAIYKRIENNSVSKQKPAFTYTRDGIKQOIGSVWFDAQTEIOA 180
 QY 181 VMEENATOVFLTSIDILEYVRSAGGENTAYVNSGSLKVLGCLPTLNEEETWCADLK 240
 DB 181 VMEENATOVFLTSIDILEYVRSAGGENTAYVNSGSLKVLGCLPTLNEEETWCADLK 240
 QY 241 CKISPIYVGLSSKTLRAVASTETAEENGFRSEKRSDPVNPYHVGSGYFAPATSANDS 300
 DB 241 CKISPIYVGLSSKTLRAVASTETAEENGFRSEKRSDPVNPYHVGSGYFAPATSANDS 300
 QY 301 ELSSDALTDMSMTDSSVGVPRYRMSKKOLOREHNRVANKGOVSLPHFRTHLPK 360
 DB 301 ELSSDALTDMSMTDSSVGVPRYRMSKKOLOREHNRVANKGOVSLPHFRTHLPK 360
 QY 361 EMPVPEPAFAELISRLKLEKLESLRHSLEERLQOIREDEKEGSEQALSSRDGAPVQ 420
 DB 361 EMPVPEPAFAELISRLKLEKLESLRHSLEERLQOIREDEKEGSEQALSSRDGAPVQ 420
 QY 421 HPLALPSSGYEDPQTLIDHLSRVLYKTGCGSPGVGRYSPRSRSDPHNNHNNQOCH 480
 DB 421 HPLALPSSGYEDPQTLIDHLSRVLYKTGCGSPGVGRYSPRSRSDPHNNHNNQOCH 480
 QY 481 TLLSTGKLPVAVACPLLGKSFLLKOTTKVHNHNTIHNNAVPTKELEAEATQVRCCL 540
 DB 481 TLLSTGKLPVAVACPLLGKSFLLKOTTKVHNHNTIHNNAVPTKELEAEATQVRCCL 540
 QY 541 CPFGTLYCYCKSKSHPKAPRLPGSGRGGLPKRNKATGEGALASADGMSA 600
 DB 541 CPFGTLYCYCKSKSHPKAPRLPGSGRGGLPKRNKATGEGALASADGMSA 600
 QY 601 AGGPOLPGEEDRSODVWOMLESEKSKSPHSAOSIKSYLSEARAPGGRVSRHLL 660
 DB 601 AGGPOLPGEEDRSODVWOMLESEKSKSPHSAOSIKSYLSEARAPGGRVSRHLL 660
 QY 661 LGASGHSRVARAHPTODPAMPPLTPPNTLAQLEACRRLAEVSPKORCCVASSQOCD 720
 DB 661 LGASGHSRVARAHPTODPAMPPLTPPNTLAQLEACRRLAEVSPKORCCVASSQOCD 720
 QY 721 RNHSAAGAGASPRFANSLAPEDHKPKKLASVHALQASELVVYFFCGEELPYRRMLKA 780

DB 721 RNHSAAGAGASPRFANSLAPEDHKPKKLASVHALQASELVVYFFCGEELPYRRMLKA 780
 QY 781 QSLTLGHEKEQLSKGNRYRYFKRASDEFACGAFFEEIMDETVLPMWEGRIILGKVERID 840
 DB 781 QSLTLGHEKEQLSKGNRYRYFKRASDEFACGAFFEEIMDETVLPMWEGRIILGKVERID 840

RESULT 2
 ID AXN2_RAT STANDARD; PRT; 838 AA.
 AC 070240;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
 DE (AXIN).
 GN AXIN2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98226558; PubMed=9566905;
 RA Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,
 RA Kikuchi A.,
 RT "Axin, a member of the Axin family, interacts with both glycogen
 RT synthase kinase 3beta and beta-catenin and inhibits axis formation of
 RT xenopus embryos.";
 RT Mol. Cell. Biol. 18:2867-2875(1998).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE AMADILLO REPEATS CONTAINED IN BETA-CATEININ.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS.
 CC -1- PPM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC EMBL: AF017757; AAC04089.1; -
 DR HSPF: P49799; IACR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 KW Developmental protein; Phosphorylation.
 FT DOMAIN 81 200 RGS.
 FT DOMAIN 327 413 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 413 478 BETA-CATENIN BINDING SITE (BY SIMILARITY).
 FT DOMAIN 469 474 POLY-HIS.
 FT DOMAIN 756 838 DIX.
 SQ SEQUENCE 838 AA: 92947 MW: 45B825C13BA07F37 CRC64;

Query Match 97.0%; Score 4310; DB 1; Length 838;
 Best Local Similarity 96.9%; Pred. No. 4.1e-236;

Matches 814; Conservative 7; Mismatches 17; Indels 2; Gaps 1;

```

OY 1 MSSAVLYTLDPSPSSFRDADAPRPVPGEGETPPCQSPVGVOSTKRPVSSNRRND 60
Db 1 MSSAVLYTLDPSPSSFRDADAPRPVPGEGETPPCQSPVGVOSTKRPVSSNRRND 60
OY 61 GLGEPEGASPDSPLTRMTKSLHSLGDQDGAYLFRFLEKREKCVDTLDFWACNGFROM 120
Db 61 GLGEPEGASPDSPLTRMTKSLHSLGDQDGAYLFRFLEKREKCVDTLDFWACNGFROM 120
OY 121 NLKDTKTLRAKAIYKRIENNSVSKOLKPKATKTYINDGKIKQOIGSMFOAQTEIOA 180
Db 121 NLKDTKTLRAKAIYKRIENNSVSKOLKPKATKTYINDGKIKQOIGSMFOAQTEIOA 180
OY 181 VMEBAVAVFLTSDIYLYEVNRSRGENTAYMNGSLKVLGCVLPTLNEEEMKCADLK 240
Db 181 VMEBAVAVFLTSDIYLYEVNRSRGENTAYMNGSLKVLGCVLPTLNEEEMKCADLK 240
OY 241 CKLSPTVVGSLSKTLRAVASTETAEENGFRKRPDPVNPYHVGSGYVAPATSSANDS 300
Db 241 CKLSPTVVGSLSKTLRAVASTETAEENGFRKRPDPVNPYHVGSGYVAPATSSANDS 300
OY 301 ELSDALTDSDSMSTDDSVGVPRYMGSKKOLQREMHRSYKANGOVSLPHFPTNRLPK 360
Db 301 ELSDALTDSDSMSTDDSVGVPRYMGSKKOLQREMHRSYKANGOVSLPHFPTNRLPK 360
OY 361 EMTPEPAFAFAELISRLKLESLERHSLERLQOIREDEKSGSDALSSRGARVQ 420
Db 361 EMTPEPAFAFAELISRLKLESLERHSLERLQOIREDEKSGSDALSSRGARVQ 420
OY 421 HPLALLPGASVEEDPQTLIDHLSRVLTQPCQSPGVGRYSRSRSDPHNNHNNHQQH 480
Db 421 HPLALLPGASVEEDPQTLIDHLSRVLTQPCQSPGVGRYSRSRSDPHNNHNNHQQH 480
OY 481 TLLSTGKLPVYACRPLGSKSLTKQTTKVNHNHYINHNNAVPKTELEATQVRCL 540
Db 481 TLLSTGKLPVYACRPLGSKSLTKQTTKVNHNHYINHNNAVPKTELEATQVRCL 540
OY 541 CRPGDYYCYCKSKSHRPARERLPGEORCGSGTLPRKNACTERGLASRDGMSA 600
Db 541 CRPGDYYCYCKSKSHRPARERLPGEORCGSGTLPRKNACTERGLASRDGMSA 600
OY 601 AGCPOLPEEGDRSDVQWQMLESERQSKSPHSAQSIKSYLESARAPGERYSRNL 660
Db 601 AGCPOLPEEGDRSDVQWQMLESERQSKSPHSAQSIKSYLESARAPGERYSRNL 660
OY 659 AGAPQLPEEGDRSDVQWQMLESERQSKSPHSAQSIKSYLESARAPGERYSRNL 658
Db 659 AGAPQLPEEGDRSDVQWQMLESERQSKSPHSAQSIKSYLESARAPGERYSRNL 658
OY 721 RNSHSAAGAGASPRANPSLAPEDHKEPKKLASVHALQASELYVTFEGCEELPYRMLKA 780
Db 721 RNSHSAAGAGASPRANPSLAPEDHKEPKKLASVHALQASELYVTFEGCEELPYRMLKA 780
OY 719 RNMHPATGQAGPTSFENPSLASEDHKEPKKLASVHALQASELYVTFEGCEELPYRMLKA 778
Db 719 RNMHPATGQAGPTSFENPSLASEDHKEPKKLASVHALQASELYVTFEGCEELPYRMLKA 778
OY 781 OSLTGHKREOLSKKGNRYVFKKASDEFACAVFEEDVTVPMYEGRTLGVERID 840
Db 781 OSLTGHKREOLSKKGNRYVFKKASDEFACAVFEEDVTVPMYEGRTLGVERID 840
OY 779 OSLTGHKREOLSKKGNRYVFKKASDEFACAVFEEDVTVPMYEGRTLGVERID 838
Db 779 OSLTGHKREOLSKKGNRYVFKKASDEFACAVFEEDVTVPMYEGRTLGVERID 838

```

[1] SEQUENCE FROM N.A.
 RA MEDLINE-99168905; PubMed-10049590;
 RA Mal M., Qian C., Yokomizo A., Smith D.I., Liu W.,
 RT "Cloning of the human homolog of conductin (AXIN2), a gene mapping to
 RT chromosome 17q23-q24."
 RL Genomics 55:341-344(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Tissue-Brain, and Lymphoblast;
 RA Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
 RA Jenkins N.A., Warburton D., Constantini F.,
 RT "Properties of mouse Axin2 and human AXIN2: chromosomal location,
 RT expression pattern, interaction with Axin and effects on embryonic
 RT axis formation."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATENIN AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
 CC TERNARY COMPLEX (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
 CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb-sib.ch).
 CC
 DR EMBL: AF078165; AAD20976.1; -;
 DR EMBL: AF205888; AAF22799.1; -;
 DR MIM: 604025; -;
 DR InterPro: IPR000342; -;
 DR InterPro: IPR001158; -;
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PRINTS: PR01301; RGS/PROTEIN.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein: Phosphorylation.
 KW DOMAIN 81 200
 FT DOMAIN 327 413
 FT DOMAIN 413 476
 FT DOMAIN 469 474
 FT DOMAIN 761 843
 FT CONFLICT 37 62
 FT CONFLICT 346 346
 FT CONFLICT 572 636
 FT CONFLICT 687 687
 FT CONFLICT 696 696
 FT SEQUENCE 843 AA; 93557 MW; F7B62BED6A4664D CRC64;

Query Match 90.6%; Score 4027.5; DB 1; Length 843;
 Best Local Similarity 89.7%; Pred. No. 3.6e-220;
 Matches 758; Conservative 31; Mismatches 49; Indels 7; Gaps 3;

```

OY 1 MSSAVLYTLDPSPSSFRDADAPRPVPGEGETPPCQSPVGVOSTKRPVSSNRRND 60
Db 1 MSSAVLYTLDPSPSSFRDADAPRPVPGEGETPPCQSPVGVOSTKRPVSSNRRND 60
OY 61 GLGEPEGASPDSPLTRMTKSLHSLGDQDGAYLFRFLEKREKCVDTLDFWACNGFROM 120
Db 61 GLGEPEGASPDSPLTRMTKSLHSLGDQDGAYLFRFLEKREKCVDTLDFWACNGFROM 120

```

```

Db 61 GLGEPGRASPSPLRTWKSLHSLGDDGAYLFRFLEREKCVDTLDFWACNGFRM 120
Oy 121 NLKDTKTLRAKAIYKRYIENNSVSKOLKPKATKTYIPDKIKKQOIGSMFOAQOTEIO 180
Db 121 NLKDTKTLRAKAIYKRYIENNSVSKOLKPKATKTYIPDKIKKQOIGSMFOAQOTEIO 180
Oy 181 VMEENAYOVFLTSIDYLEVRSNGENTAYMSNGLSLKVLCGYLPTLNEEEMTCADK 240
Db 181 VMEENAYOVFLTSIDYLEVRSNGENTAYMSNGLSLKVLCGYLPTLNEEEMTCADK 240
Oy 241 CKLSPTVGLSKTLRATASVSTEAENGFSFRKSDPVNRYHNGSGYVAPATISANDS 300
Db 241 CKLSPTVGLSKTLRATASVSTEAENGFSFRKSDPVNRYHNGSGYVAPATISANDS 300
Oy 301 ELSSDALTDMSMTDSSVDGVPPYRMGSKKOLQREMHRSVANGOVSLPHFPTTHRLPK 360
Db 301 ELSSDALTDMSMTDSSVDGVPPYRMGSKKOLQREMHRSVANGOVSLPHFPTTHRLPK 360
Oy 361 EMTPEPAFAFAELISRLKLEKLEESRHSLEERLQOIREDEREGSEQALSSRDGAPV 420
Db 361 EMTPEPAFAFAELISRLKLEKLEESRHSLEERLQOIREDEREGSEQALSSRDGAPV 420
Oy 421 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHHHOCCH 480
Db 421 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHHHOCCH 480
Oy 481 TLSTGKLPVVA---ACPLIGKSFLLKQTKKHVHHNHVHHNAVPKTEIEAEATOR 536
Db 481 TLSTGKLPVVA---ACPLIGKSFLLKQTKKHVHHNHVHHNAVPKTEIEAEATOR 536
Oy 537 VRLCPGSDYCYCKSKSHRPARPLRPGQSGRSTLKRNAKGTPEGLASAROGG 596
Db 537 VRLCPGSDYCYCKSKSHRPARPLRPGQSGRSTLKRNAKGTPEGLASAROGG 596
Oy 599 ARGGAGALQLPREBGRSQDYWMWMLSEBOSKPKPHSAOSTKAYPLRESARSSPGEAS 658
Db 599 ARGGAGALQLPREBGRSQDYWMWMLSEBOSKPKPHSAOSTKAYPLRESARSSPGEAS 658
Oy 657 RHHLIGA-SGHSRSVAAHNPFTODPAMPRLPPTLAOLEFACRRLAEVSKPOROCVVA 715
Db 657 RHHLIGA-SGHSRSVAAHNPFTODPAMPRLPPTLAOLEFACRRLAEVSKPOROCVVA 715
Oy 716 SQGDRNHSAGOGASFPANPSLAPEDHKPKKLASVHNAQASELVYTFPGCEELPYR 775
Db 716 SQGDRNHSAGOGASFPANPSLAPEDHKPKKLASVHNAQASELVYTFPGCEELPYR 775
Oy 776 RMLAQSITLGHFEQSLSKGNRYTFKKASDEFACGAVEEIDETVLPMYGRITLIG 835
Db 776 RMLAQSITLGHFEQSLSKGNRYTFKKASDEFACGAVEEIDETVLPMYGRITLIG 835
Oy 836 VERID 840
Db 836 VERID 840
Oy 839 VERID 843
Db 839 VERID 843

```

```

RA Bae Y.-K., Hibi M., Hirano T.:
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish."
RL Mech. Dev. 91:293-303(2000).
CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB032263; BA092440.1; -.
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342; -.
DR InterPro: IPR001158; -.
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS0132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 84 203
FT DOMAIN 329 415
FT DOMAIN 415 467
FT DOMAIN 412 419
FT DOMAIN 730 812
SQ SEQUENCE 812 AA; 91496 MW; 4655ADA6DE2240CC CRC64;

Query Match 59.2%; Score 2632.5; DB 1; Length 812;
Best Local Similarity 62.1%; Pred. No. 1,8e-141;
Matches 535; Conservative 88; Mismatches 154; Indels 85; Gaps 15;

Oy 10 LPDPS-SFREDAPRPVPEGEETPCQPSVGKOSTRPM-PVS-----SNARNE 59
Db 5 LTPMWSFREDPRPPVPEGEETCHHPS--KLMMRPKDPVKITMADLRKSTAROE 62
Oy 60 DGLGEPGRASPSPLRTWKSLHSLGDDGAYLFRFLEREKCVDTLDFWACNGFRM 119
Db 63 DGLGEPGRASPSPLRTWKSLHSLGDDGAYLFRFLEREKCVDTLDFWACNGFRM 122
Oy 120 MNLKDTKTLRAKAIYKRYIENNSVSKOLKPKATKTYIPDKIKKQOIGSMFOAQOTEIO 179
Db 123 MNLKDTKTLRAKAIYKRYIENNSVSKOLKPKATKTYIPDKIKKQOIGSMFOAQOTEIO 182
Oy 180 VMEENAYOVFLTSIDYLEVRSNGENTAYMSNGLSLKVLCGYLPTLNEEEMTCADL 239
Db 183 VMEENAYOVFLTSIDYLEVRSNGENTAYMSNGLSLKVLCGYLPTLNEEEMTCADL 242
Oy 240 CKLSPTVGLSKTLRATASVSTEAENGFSFRKSDPVNRYHNGSGYVAPATISAND 299
Db 243 KAKALATVVGLSAKTLR-SPLRAVADALKGYRSTRSDPGRNPTSGYSPAPATISAND 301
Oy 300 ELSSDALTDMSMTDSSVDGVPPYRMGSKKOLQREMHRSVANGOVSLPHFPTTHRLPK 359
Db 302 ELSSDALTDMSMTDSSVDGVPPYRMGSKKOLQREMHRSVANGOVSLPHFPTTHRLPK 361
Oy 360 KEMTPEPAFAFAELISRLKLEKLEESRHSLEERLQOIREDEREGSEQALSSRDGAPV 419
Db 362 KEMTPEPAFAFAELISRLKLEKLEESRHSLEERLQOIREDEREGSEQALSSRDGAPV 416
Oy 420 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHHHOCCH 479
Db 417 HPLALLPSGSYEEDPOTLIDHLSRVLTGPGQSPGVGRSPRSRPHHHHHHOCCH 468

```

```
OY 480 HTLSTGCKLRPVACRLLG---GKSFLLKOTYKHHNHYTHHHNAVPTKEIEAEATOR 536
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 469 ---LPRGSLSTRSSSSNGVYPAKTFISRSTSTHHNHHNAGPKSKOEIVATOR 525
OY 537 VRCLSPGSTDVYCYCKSKSHKAPERYLPGEGCS-----RGCTLPKR-----NA 581
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 526 VOCLCHG-----TSECTAPYIKRSRLGRDQASPAVALGHSSTLSKRLCKSGEENV 579
OY 582 KGTPEGLALNARDGMSAAGCPOLPCEEGRSDDVWOMMLESEKRSKSHASQSTIKS 641
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 580 EGLENSL-----OLPADSTDRSONWOMLIESROTKHKHSTONVKS 624
OY 642 YPLESARAAPERGVSRHHL---GASGHSRVARANPPTODAPRPLRPPTLQOLEEAC 698
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 625 HSELPRT-----HTWGGSSGHLRAHNPAPVDPAPRPLRPPTLQOLEEAR 675
OY 699 RRLAEVSKPOKRCVSAQOORNRHNSAAGQASPFANPSLAPEDHKPKKLASYHALQA 758
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 676 RRLAEVSKPKORHSTSLORDKSHPVVONGSAF-----PMBERKDPKMSGCHSLG 730
OY 759 SELVYVYFPGGEELPYRMLKAOSLTGLHFEKQLSKGNRYRYFKKASDEFACGAVEEI 818
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 731 SELVYVYFPGGEELPYRMLKTHSLTGLHFEKQLRKGNRYRYFKKASDEFECAVPEEV 790
OY 819 WDETVLPMYEGRLGKVERID 840.
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 791 WDCVTLPMYEGKILGVRMD 812

RESULT 5
AXN_CHICK
ID AXN_CHICK STANDARD; PRT: 841 AA.
AC 042400;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN).
OS AXIN OR AXN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97373830; PubMed=9230313;
RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
RA Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F., Perry W.L. III,
RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
RT pathway that regulates embryonic axis formation."
RL Cell 90:181-192(1997).
CC -|- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOSOL; PLASMA MEMBRANE (BY SIMILARITY).
CC -|- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.
CC -|- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC -|- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF009012; AAC60245.1;
DR HSSP; PA9799; IAGR.
```

```
DR InterPro; IPR000342;
DR InterPro; IPR001158;
DR Pfam; PF00615; RGS; 1.
DR Pfam; PF00778; DIX; 1.
DR PROSITE; PS50132; RGS; 1.
KW Developmental protein; Phosphorylation.
FT DOMAIN 88 211
FT DOMAIN 348 433
FT DOMAIN 434 508
FT DOMAIN 759 841
FT SEQUENCE 841 AA; 94931 MW; 400D0C90E72506EE CRC64;
SO QUERY MATCH 39.1%; Score 1736; DB 1; Length 841;
Best Local Similarity 44.5%; Pred. No. 7.4e-91;
Matches 406; Conservative 128; Mismatches 214; Indels 164; Gaps 35;
OY 12 DPSSFEEDARPRPVGEGEPQSVGKYSTKPRPV-----SNARNEDG--- 61
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 11 DLGRSFTEDARPRPVGEGE-----LVSTDPRPVSHGFYSKSDAVRNSTSTAT 60
OY 62 -----LG-EPEGRASPSPLRTWTKSLHSLGDQDAULFRTFLEREKCVDTLDFWA 113
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 PRSOLDLGYEPREGSASPTPYLKMAESHLDDQDQINLFRFLKQDDCADLDFWA 120
OY 114 CNGFRQMN---LKDTKLVAKAIYKRYT-ENNSVYSKQLKPAKTYTRDGIKKOIGSV 169
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 121 CSGFKLEPCVSNEEKRLKAKAIKYKYLIDNNGIVSRQIKPATKSFYKDCVMKLOIPD 180
OY 170 MEDQAOETLOAVMEENAQVLFISDILEYVRSGEENAYMS--NCGISLKVLCGYLT 227
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 181 MEDQAOETLOAVMEENAPFLFLKSDILEYTRTGEGSKYISDPGSGTGLGYLT 240
OY 228 LNEEEMTC-ADLKCKLS-----PIVGLSKTLRATASVSTETAE---NGFRSFKRSD 278
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 241 LNEDEWKCDQDTEPEASRDSAPS-SRLQKLLTETAQORATSTRYSEGRFRGSMRE 299
OY 279 PVNRYHVGSGYVAPATANDSE---LSSDALTDSSKMTSSVDGVPRYMGSKKQLO 335
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 300 PVNRYVYVGYAMAPATANDSEQSSMSDA---DTMSLTGSSIDGIPRYRL--RKQHR 354
OY 336 EMNRKANGOVSLPFRTRHLPKEMTVPRPAFAELISLTKYLESRHSLERL 395
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 355 EMQESAKANGRPLRLPRTIRYRMPKDT-NVEREKALIELINLEVOEKREAEKLEERL 413
OY 396 QOIREDEKESSQALSSRDGAPVONRLALPSC-----SYEE 433
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 414 KVRAREE---GEADDISGPSVISHK---MPSAQRYNPAFRYSEMGACAGQMRDANE 467
OY 434 DPQTLDDHLSRYLTKRCCSGVGRYSPRSRPNHNNHNNHNNHNNHNNHNNHNNHNNH 493
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 468 NPESLIDHNVORVMKTPCOSCGRHSRSPKRPSPESGH-----LGLSLGLTTP-- 518
OY 494 ACPRLGSGSLPLKQTT-----KHNNHYTHHHNAVPTKEIEAEATORVCLRG 543
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 519 -----GHCKHTTKSGMKLDANLYNHNKHYTHN-THHSHMKKEQIEDATQVONSTRW 572
OY 544 GTDYVYC-SKCKSHPK---APRLPGEOFGCSRGGLTPKRNAKTEGRLASARDGMS 598
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 573 NVDSHNVYTKSRYSENLGMAVPMDSLGYSG-KASLLSKRNKIKKTDGSKS---DGANY 627
OY 599 SAAGCPOLPCEEGRSDDVWOMMLESEKRSKRPASQSTIKSYPLESARAAPERGER- 654
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 628 EMPGSP---DEVENQKILQMIIEGEIKSNKTKTNGSSGVKQLSDIWRPLSIERP 683
OY 655 VSRHHLGASGHSRVAR-APFTODPAMPRLPNTLQOLEACRRLAEVSK-----PQ 708
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 684 VAVNHWV---SAQLRVVQPSHPFIDPMPRPAPRNPRLQLEAKRRLLEEKRKAGKPL 741
OY 709 KORCCVASQOORNRHNSAAGQASPFANPSLAPEDHKPKKLASYHALQASELVYVYFPC 768
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 742 KOR-LKPKR-----PGSGASPCEN-----IVAVYVFC 769
```

QY	769	GEPIPRMFLAOSTLTLCHFEOLSKGNRYRKRKSDENACGAVEIMDETVELPMY	828
Db	770	GEPIPRVLNAGRVYTLGQFFKELLTKGNRYRKRKSDENACGAVEIMDETVELPMY <td>829</td>	829
QY	829	EGRLGKVERID	840
Db	830	EKLIIGVERIKID	841
RESULT	6		
AXNL_RAT			
ID	AXNL_RAT	STANDARD:	PRT: 893 AA.
AC	070239;		
DT	01-OCT-2000 (Rel. 40, Created)		
DT	01-OCT-2000 (Rel. 40, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	AXIN1 PROTEIN (AXIS INHIBITION PROTEIN 1) (AXIN) (FRAGMENT).		
OS	AXIN1 OR AXIN.		
OS	Rattus norvegicus (Rat).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
NCBI_TaxID	10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	MEDLINE-98151361; PubMed-9482734;		
RT	Iheda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi A.;		
RT	"Axin, a negative regulator of the Wnt signaling pathway, forms a		
RT	complex with GSK-3beta and beta-catenin and promotes GSK-3beta-		
RT	dependent phosphorylation of beta-catenin.";		
RL	Embo J. 17:1371-1384(1998).		
CC	- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES		
CC	BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-		
CC	CATENIN AND APC BY GSK-3B (BY SIMILARITY).		
CC	- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION		
CC	BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS		
CC	CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO		
CC	PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).		
CC	- SUBCELLULAR LOCATION: CYTOSOL; CYTOSOLIC (BY SIMILARITY).		
CC	- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG		
CC	FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,		
CC	SPLEEN AND LIVER.		
CC	- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY		
CC	PP2A (BY SIMILARITY).		
CC	- SIMILARITY: CONTAINS 1 RGS DOMAIN.		
CC	- SIMILARITY: CONTAINS 1 DIX DOMAIN.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb.ch/announcement/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: AF017756; AAC40066.1; ALT_INIT.		
DR	HSSP: P49799; IAGR.		
DR	InterPro: IPR000342; -		
DR	InterPro: IPR001158; -		
DR	Pfam: PF00615; RGS; 1.		
DR	Pfam: PF00776; DIX; 1.		
DR	PROSITE: PS01332; RGS; 1.		
DR	developmental protein; Phosphorylation.		
FT	NON_TER	1	
FT	DOMAIN	154	277
FT	DOMAIN	414	498
FT	DOMAIN	499	567
FT	DOMAIN	811	893
FT			DIX.
QO	SEQUENCE	893 AA; 99188 MW; 3CCBD224EDD384C CRC64;	

Query Match 37.48; Score 1661; DB 1; Length 893;

QY	12	DPSSFFEDAPRRPVGEEGE-----TPRCQSPV--GKYQSTKPMYSSNARNREDIG-	63
Db	77	DLGASFFEDAPRRPVGEEELVSTDSRPVNHSCGSGKSTKSESTATPRPSDLDTG	136
QY	64	EPBGRASPDRLPRMTKSLSHLLGDGGAVLFETFLERKGCYDTLDFWACGSPOMNIK	123
Db	137	EPBGASAPRRPYLRMAESHLSDDDGSLRFTFLKQSGCADDLDFWACSGFKLEPC	196
QY	124	DT---KTLRAKAIKYRT--ENNSVVSOKDKPATKYTIDGJIKQOIGSMEDAOATEIO	179
Db	197	DSMEERKLKLAIRYKRYKLLIDNSNGVSRQTKPATKSFIDCYVMKQOIDPAMPDAQOTEIO	256
QY	180	AAVEENAAUYELFSDLYLEVYVSGGENTAVMS--NGCGLSLVLGSLYPLTLEEEEMTC-	236
Db	257	STMEETUYISFLKSDIYLETYRTGSESPKVCSDQSGSTGSGMGSYPLTLEDEEMDCD	316
QY	237	-----ADLKCKLSPTVVLGSSKTL-----RATAVSRTETANGFRSKRDPAPRYNV	285
Db	317	QDADEDDGDDSVPPS--RLTQKLLLETARAPASSRRRYNEGRELRYGSMR--EPVNPYYV	372
QY	286	GGGVVAPARPTANDSE---LSSDALDMSMTSDSVGCVPRYVNGSKKOLORENNHNVK	342
Db	373	NSGYALARPATSAHDSFOGLSSDA---DLTSLDSSVVGIIPEYK--RKHNRHEQESVE	427
QY	343	ANGQVSLRPFRTNRLPKMTPEVERAAFAELISLEYKLTLELSHSLERLQOIREDE	402
Db	428	VNGRYVLRPIPRTRYKPIR--VERQKFAEELILVAVQRTREMEKLEERLKYRME	486
QY	403	EKEGSQLASSDQAPVQNPRLALS-----GSYEDPOTITIDHLSR	445
Db	487	EKGDEGMP---SGMASTKLEPSVAMNHRFRRYVDMGCSGLRANHENPESILDENYOR	542
QY	446	VLTETPCOSPVGYRYSRPSRSPDNHNNQOCHTSLTSGKLRYVAACPDLSG----	500
Db	543	VMTREGCCQSPG-----PGRHSPDSGH-----YAKTAVLGGTASGH	577
QY	501	-----KSPFLTKQT---KVNHNHYNNHNAVPTKEIEAATQRYKSLRGSTDYUCY	550
Db	578	GKHAERKLGKIDLSAGLHNHRYNHN--VHNNSA--PRKEOMEAEARVQSSPSWGRPTNGH	635
QY	551	SKCKENPKA--PEPLRGDQFGSGRGCTLPKKNAPGTEGLTSLASRDGMSAAGROLPG	608
Db	636	AKPRYSIESGTGNPAGDLAFGKASAPSKNTKAESEGNASA-----EVPSS	683
QY	609	--EEGDSQDVWQMLLESERO--SKKPNHSAOSIRKSYPLESARAAGERVSNHNLGA	663
Db	684	TTEDEAKNOCKIMQWILEGEKEISRHRKAGHSGSMQRQOAHESRPLSIRBPAGVHNHWS	743
QY	664	SGHSHSVARAHPTODPAMRPLTPRNTLQOLEEACRYLAESKQAKOORCCVAAQORDRNH	723
Db	744	AGLRNSVDPSHLFTODPMPRPNRPNPLTOLEEARRRILEEKKRANK--LPSKORTKSQ	800
QY	724	SAAQAGASPRAPNSLAPEDHKEPKKLASVHALDASELVYVTPFGCEGTIRYMLYKASQSL	783
Db	801	RKAGGGSAP-----CDSIVAIYATFGCEPIRYTLTVKRAAV	836
QY	784	TLGHFKEOGLSKGNRYRYFKKASDEFAAGVFEETWDETFLVRYEGRLIGKVERTID	840
Db	837	TLGQFKELTLLKKSGSYRYFKKVSDEFQGVFEVREDEALTLVFEFKITGKVEKD	893

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA MEDLINE=9373830; Pubmed=9230313.
 RX Zeng L., Fagotto F., Zhang T., Hsu W., Vasicsek T.J., Perry W.L. III,
 RA Lee J.J., Tligman S.M., Gumbiner B.M., Costantini F.;
 RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
 RT pathway that regulates embryonic axis formation.";
 RL Cell 90:181-192(1997).
 CC -1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
 CC BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMD/BDL REPEATS
 CC CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
 CC PLAKGLOBIN (GAMMA-CATENIN), APC, DVL AND PR2A (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOSOL/PLASMA (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
 CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.
 CC -1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PR2A.
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF009011; AAC53285.1; -.
 DR HSSP: P49799; IAGR.
 DR MGD: MG1:1096327; Axin.
 DR InterPro: IPR000342; -.
 DR InterPro: IPR001158; -.
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein; Phosphorylation; Alternative splicing.
 FT NON_TER 1
 FT DOMAIN 10 18 POLY-ALA.
 FT DOMAIN 217 340 RGS.
 FT DOMAIN 477 561 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 562 630 BETA-CATENIN BINDING SITE (BY
 FT SIMILARITY).
 FT DOMAIN 910 992 DIX.
 FT VASAPLIC 860 895 MISSING (IN ISOFORM 2).
 SO SEQUENCE 992 AA; 109917 MW; 70EBB53D387BD26F CRC64;

Query Match 37.28; Score 1655; DB 1; Length 992;
 Best Local Similarity 42.78; Pred. No. 3.4e-86;
 Matches 390; Conservative 133; Mismatches 246; Indels 144; Gaps 30;

OY 12 DPSSSFREDARPPVPEGE-----TPCQPSV--GKVSQKRPVSNARNRNDGIG- 63
 DB 140 DLGASFTDARPPVPEGEELGVSTDSRPVNHSPGSGKGTSTKSTSTATPRKSLDGLG 199
 OY 64 EPEGASPDSPFLRWTKSLHSLDQDGAULFRFLEREKCVDTLDFWAFACNGFRQMLK 123
 DB 200 EPESASPTPYLRMAESLHSLDDQGISLFRFLKQEGCADDLDFWAFACSGFRKLEPC 259
 OY 124 DT---KILRAVAKATYKRI-ENNSVVSQQLPATYTIYRDGKKKQOIGSVMDQATQTEQ 179
 DB 260 DSNERRKLARATYKRIYLDNSGIVSRQTPATKSFKDCVMKQOIPAMPDOATQTEIO 319

OY 180 AVMEENAYQVLTSDIYLYEVRSGGENTAYMS--NGGLSGKVLGCLYPTLNEEEMTC- 236
 DB 320 STMENYTPSLKSDIYLYETRTGSESPKCSDDSGSGTGKMSGYPTLNEDEEMKCD 379
 OY 237 -----ADLKCKLSPYVGLSSKTL-----RATASVSTETAEENFRSEKSDPVPNRYH 285
 DB 380 QDADDDCRODLPSP-RLTQKLLLETAAPAPSSRRYNEGELLYGSMR--EPNPNRYV 435
 OY 286 GSGYFAPATSANDE---LSSDALTDMSKMTDSSVDCVPPRYMGSKKOLQREHNSVK 342
 DB 436 NSGYLAPATSANDEQOSSLSDA---DTLSLTSVSGIIPYRI--RKONHREMEISIO 490
 OY 343 ANGOVSLPHFRNTLREKMPVPERAFARAEISLTKLELSEHNSLEPRLQIRDE 402
 DB 491 VNGRPLRPHRTYMPKEIR-VEROKFAEELHLEAVQRTREKEELEERLAKVRME 549
 OY 403 EKEGSEQALSSRDGAPVONPLALPS-----GSYEEDPOTLIDHLSR 445
 DB 550 EGEDEEMF-----SGFMASHKLPYRAMNHFRRYVDMGCSGLRYAHENPESILDEHYOR 605
 OY 446 VLKTPGCSQPGYGRISPRKSRSDNNHNNQOCHTLSTGSKLPVYACPLG- 500
 DB 606 VMKTPGCSQPG-----PGRHSPDSGH-----VAKTAVLGSTASGH 640
 OY 501 -----KSLFTQQT-----KHVNHVHNNAVKTKEIEAEATQVRCLCPGSTDYCY 550
 DB 641 GKNVPRKLGKLDLTAGLNNHNNHNNH--VHNSA--RKEDMEAVARRVOSSPSGETGCH 698
 OY 551 SKCKSHPK-AREPL-RGBOFGSGRGGLTKRNKSTERGLSARDGMSAAGSPOLRG 608
 DB 699 AKPRYSYNAGTTLAAGDLPRFGKTSAPSKRYTKKAESGKNNA-----EYPS 746
 OY 609 --EEDRSQDWMQMLSEDRQ--SKSRPHASQSTKSTPLESAAAGGERYSRHHLLGA 663
 DB 747 TTEDEKQOKMOWLIEBEKETSRHKAHGSSGLRKQDANSSRLSTERGAIVPWS 806
 OY 664 SGHSRSVARHPFTQDPMPRLTPPNTLAQLEAEACRLAEVSK-----POKORCVASQ 718
 DB 807 AOLRNSVQPSHFLIDPMPRPAPRPALPQLDEARRRLEEEKRANKRPSKRYVOAVMO 866
 OY 719 RDRNHSAGQACASFPANP-----SLAPDHEKPKKLASVHALQASELVYTFE 767
 DB 867 R-----GRICVRPACAPVLSVPAVSDLESETETKSQRKAGGSAPPCDSIYGYF 919
 OY 768 CGEELPYRMLKAOSLTGHEKEOLSKKGNRYTKKASDERACGAVPEIIDDDELPRM 827
 DB 920 CGEIPRYTLVNGRAVTLGQFKELLTKKGSYKRYKVSDEFDCGVPEEVEDEPVLV 979
 OY 828 YEGRIIGKVERID 840
 DB 980 PEEKIIGKVEKD 992

RESULT 8
 AXN_XENLA STANDARD; PRT; 842 AA.
 ID AXN_XENLA
 AC 09YGYO;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN (AXIS INHIBITION PROTEIN) (XAXIN).
 GN AXIN OR AXN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99173782; Pubmed=10072781.
 RA Hedgepeth C.M., Deardorff M.A., Klein P.S.;
 RT "Xenopus axin interacts with glycogen synthase kinase-3 beta and is
 RT expressed in the anterior midbrain.";

```

RL Mech. Dev. 80:147-151(1999).
CC - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC - DEVELOPMENTAL STAGE: WEAKLY AND UBQUITOUSLY EXPRESSED THROUGHOUT
CC MESENTERIAL ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
CC - PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF097313; AAC71036.1;
DR HSSP: P49799; IAGR.
DR InterPro: IPR000342;
DR InterPro: IPR001158;
DR Pfam: PF00778; DIX; 1.
DR Pfam: PF00778; DIX; 1.
DR PROSITE: PS01332; RGS; 1.
DR Developmental protein; Phosphorylation.
FT DOMAIN 88 211 RGS.
FT DOMAIN 348 433 GSK-3B BINDING SITE (BY SIMILARITY).
FT DOMAIN 434 508 BETA-CATENIN BINDING SITE (BY
FT SIMILARITY).
FT DOMAIN 760 842 DIX.
FT SEQUENCE 842 AA; 94459 MW; BDA152734C97191E CRC64;
Query Match 37.28; Score 1654.5; DB 1; Length 842;
Best Local Similarity 42.58; Pred. No. 3e-86;
Matches 385; Conservative 125; Mismatches 246; Indels 149; Gaps 28;
QY 12 DPSSFFEDAPRPVPEEGE--TPPCOPSVGKQSTKPMV-----SSNARNEDELG 63
DB 11 DLGSEFEDAPRPVPEEGELITTDPRPSHTYSLKNDGKIKWTSFARPRDLGLG 70
QY 64 EPERASPDSPFLRWTSLSHSLDODGAYLFTLEREKCVDTLDFWACNGFRQMLK 123
DB 71 EPERASPDSPFLRWTSLSHSLDODGAYLFTLEREKCVDTLDFWACNGFRQMLK 130
QY 124 DTKT---LRVAKATYKRYI--ENNSVVSOKLPATKTYIRGDIKQOIGSVNFOAQTEIQ 179
DB 131 DSKVERKLAKAKIKKYVLDNSGIVSKQIKPATKSTFKCVALRQOQIDPAMFOAOEIQ 190
QY 180 AVMEENAYQVFLSDIYLEVRSRGENTAYMS--NGGLSLKYLKCYLPTLINEEEMTC- 236
DB 191 SMEDNTNYPFLKSDIYLETITGGESPKYVSSQSSSGTGKPSGLPTPLNDEEMRC 250
QY 237 -----ADLKC--KLSPTVYVGLSKLRATYASTETAEANGFRSKRSDPVNPHVGS 287
DB 251 QGGEHERERCIPSSLSFQKRLADSSSHCAGSNRRSLDGRE--FRPGTWREPNVYVNT 308
QY 288 GYFAPATYSANDE--LSDALTDMSMTDSSVDGVPYRMGSKQOQREHRSVKAN 344
DB 309 GYVAGAVTYSANDESSQSSMSDA---DTMSLTDSVDCIPIYRL--RKHYRREQESANAN 363
QY 345 GOVSLFHPFTRHLPKEMTPVEPAFAELISRLKLESLERHSLERLOQIREDEK 404
DB 364 GRPLPDIHRTYHMPKDI--HYDEKFAELISRLLEVLDREAEQLEERIKRYAE-- 420
QY 405 EGSEQALSSRDGAPVQHPLALPSG-----SYEDPQTLTDH 442
DB 421 EGDDGVSSGSPV-ISHK---LPSGPMHFNHSRYSETGCVGQIIDAHEENDESLIDH 476

```

```

QY 443 LSRVLTGPGCSPGGRYGRSPSRSDHHO-----HHHQOCHTLSTGGKL 489
DB 477 VQVRKVTGCGSPGGRSPKSRSDGHLSTPLGSLTMOGTGKHSKSTAKVDSGNL 536
QY 490 PVVACPLLGSKFELTKOTYRHHVHHVAVPTKEIEAEATORYRCCLPGGTGYC 549
DB 537 -----HHHKVYHH-VHHIGYKPKQIDIGESTOKOTNFPNNVSHN 578
QY 550 YSK-----CKSHPRAPDEPLPEQFCGSGTLPYRNKAGTEPGLALARDGMSAAGP 604
DB 579 YATSRNVAEEMGAPNPMDSLAYSQ--KVSMLSRNKAADLGRKSESA-----SHEMP 630
QY 605 QLPGEGRSDVQWMMLESERO--SKSRHNSQSTKSTPLESARAAGEERSHLL 661
DB 631 VVP-EDSRHKKILQWIEGKEKILRHKSNSHSSAKKOPTELARPLSIERGAVHP 689
QY 662 GASGHSRSVARHPTDPPAMPPLTPPTLAQL-EACRRLAEVSK-----POKORCVA 725
DB 690 VSAQLRNVPQSPHFIDPMPRPAPNPLQLVSKGARGLEBEKKAAMPOKRL--- 746
QY 716 SQQRDRHNSAAGAGASFPANPSLAPEDHKEPKKLASVHALQASELVYVYFCGEIPIYR 775
DB 747 -----KPOKKMVSAPQPCDNIYVAYYFCGEPIPYR 777
QY 776 RMLKASLTIGHFEKQSLKKNRYEYFKKASDEFACGAVEEIMDETVLPMTEGRILK 835
DB 778 TMVGRVYTLGQFRELITKGNRYRYFKKYSDEFDCGVVEEVEDMILPIYEKTIQ 837
QY 836 VERID 840
DB 838 VERID 842
RESULT 9
AXNI_BRARE STANDARD; PRT; 835 AA.
ID AXNI_BRARE
AC P57094;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN 1 (AXIS INHIBITION PROTEIN 1).
GN AXIN1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171051; PubMed=10704853;
RA Shimizu T., Yamanaoka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT *Cooperative roles of Bozozok/Pharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish."
RT Mech. Dev. 91:293-303(2000).
CC - FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CC CATEININ AND APC BY GSK-3B (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC - PFM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
CC PP2A (BY SIMILARITY).
CC - SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC - SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB032262; BAA92439.1;

```

DR HSP: P49799; IAGR.
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein: Phosphorylation.
 FT DOMAIN 92 214 RGS.
 FT DOMAIN 351 436 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 437 512 BETA-CATENIN BINDING SITE (BY SIMILARITY).
 FT DOMAIN 753 835 DIX.
 FT SEQUENCE 835 AA; 94351 MW; 1C62FC1F5937C87 CRC64;
 Query Match 36.68; Score 1628; DB 1: Length 835;
 Best Local Similarity 43.18; Pred. No. 9.2e-85;
 Matches 388; Conservative 128; Mismatches 243; Indels 142; Gaps 33;
 7 VTLDPSSSFREDAPRPVPGEGEPGCPSP-----VGKYSTKPMVSSNARNE 59
 10 ICYLPDLGSSFTEDAPRPVPGEGDLVSSDGRQYNSFYSSKSDSLKNESIATPRPD 69
 60 DGLG-EPEGASPSPLRTWTKSLHSLGDGAYLFTFLERKCYDTLDFWFCNGFR 118
 70 LDLGEPGASPSPLRTWTKSLHSLGDGAYLFTFLERKCYDTLDFWFCNGFR 129
 119 OMNLRD--TKLRVAKAIYKRYT--ENNSVSKOLKPRATKTIIRGICIKOOIGSVFDOAQ 175
 130 KOEANDENEMKLAKAIYKRYTLDNNGITVSQIKPATKSEIKOCVMKLHIDPMFDOAQ 189
 176 TEIOVMEENAYOVLTSIDILEYVSGENTAYMSNG--LGSILKYCGYLTPTNEEE 233
 190 TEIOTMEENYPLFLKSDILEYTRTGESPKLFSDOSSVSGNKYPLGLPIYIEVE 249
 234 WTCADLKCLSL--PTVVG-LSSKTL-----RATASVSTETAEENGSRFSKSDPNVY 283
 250 WRQDEEQIADSPTEPSNRLTKLLETVPQVANSKRYODNRE--YRHASWREPNVY 307
 284 HVGSGYFAPRTSANDF--LSSDALDLDMSMTSDSVDCVPRYMSKQOLOREHRS 340
 308 YVNGVALAPRTSANDSQOQSSDA--DTLSLTDSSVDCVPRYR--RKPHREIHES 362
 341 VKAGOVSLPFRPTNRLPKEMTVEPAPAFALISRLKLEKLESHSHSEERLOQRE 400
 363 AKVNGRPLPFRPTNRLPKDI--HYERKFAELISRLGLEVLREKREOKLEERLAKRRL 421
 401 DEEREGSE---QALSSRDGP--VOHPLALLPSGSY-----EEDPOTILDDHLS 444
 422 EEEGDADISTGPSLANHRYPAVHYGYGRYSMSYNGQLRDHNEPESILDEHYQ 481
 445 RVLTTPGCGSGVGRYSRSPDHNNHNOOCHTLLSTGKILPRPAACPLAGK-SF 503
 482 RVMTPTGCGSGTGRHSKRSRPG-----LRAGKTPGI-MMPILSGGQCKH 526
 504 LTKOTTK---HVNNH-YIHH---HAYPKTEETEAETORVRLCPG---TDYUCYS 551
 527 QARCGPRGEALHNHNKHTHTHAAAGKPKQAEAEAR-----MRGFPANTEQHNYG 581
 552 -KCKSH-----PKAREPLDEGFCGSRGCTLPKRNAKTEPGLALSARDGMSAAG 603
 582 PKSRNYADGMSVGRNTMDPMG---YSSKSGTSLSKRPVKEDGDNFEMRE----- 628
 604 POLGEEEDRQSDVOMWMLSEBROS--KSKPH-SAQISIKSYPLESKRAAPGERSHH 659
 629 -PLPADDERMOKILOMMEEKEAGRYKSPYSGISGPKAOGHEPARSPSSVLAHV 687
 660 LLAGSGHSRVARAPFTQDAMPPLTPPNTLAOLEEACRRLAEVSKQOKRCCVAAOOR 719
 688 PWVTAQLANNVQPSHPFQDPTMPNPAPNDLTGLEARRLEF----- 731
 720 DRNHSAGQAGAPFANPSLAPEDHKEPKKLASVHALQASLAVTYFFCGEETIPRYMLK 779

Db 732 ERRKSGTLQ-----AKORHKNMKK-----QPCENTVAYVFCGEPIRYFSVK 774
 QY 780 AQSLLGHFKQLSKKGNRYRYFKKASDEPACGNFEEIMDEVLTPYDEGRILCKVRI 839
 Db 775 GRVTLGGFKELTKKSGYKFKVSEFGGVFEEVEDDALPLFEERIKGVEKV 834
 QY 840 D 840
 Db 835 D 835
 RESULT 10
 AXIN1_HUMAN
 ID AXIN1_HUMAN STANDARD; PRT; 900 AA.
 AC 015169;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE AXIN1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
 GN AXIN1 OR AXIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP MEDLINE=97373830; PubMed=9230313;
 RA Zeng L., Fagotto F., Zhang T., Hsu W., Vasticek T.J., Perry W.L. III,
 RA Lee J.-J., Tilghman S.M., Gumbiner B.M., Costantini F.;
 RT "The mouse fused locus encodes Axin, an inhibitor of the Wnt signaling
 RT pathway that regulates embryonic axis formation.";
 RL Cell 90:181-192(1997).
 CC -!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
 CC BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
 CC CATENIN AND APC BY GSK-3B.
 CC -!- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
 CC AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
 CC OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
 CC TERNARY COMPLEX. MAY ALSO BINDS TO PLACOGLOBIN (GAMMA-CATENIN),
 CC APC, DVL AND PP2A.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
 CC -!- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
 CC PP2A.
 CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 DIX DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF009674; AAC51624.1; -
 DR HSP: P49799; IAGR.
 DR MM: 603816;
 DR InterPro: IPR000342; -
 DR InterPro: IPR001158; -
 DR Pfam: PF00615; RGS; 1.
 DR Pfam: PF00778; DIX; 1.
 DR PROSITE: PS50132; RGS; 1.
 DR Developmental protein: Phosphorylation.
 KM NON_TER 1 1
 FT DOMAIN 125 248 RGS.
 FT DOMAIN 385 470 GSK-3B BINDING SITE (BY SIMILARITY).
 FT DOMAIN 471 540 BETA-CATENIN BINDING SITE (BY SIMILARITY).
 FT DOMAIN 818 900 DIX.
 FT SEQUENCE 900 AA; 99803 MW; E5F990B11FC7B3B CRC64;


```

Query Match      36.1%; Score 1605; DB 1; Length 900;
Best Local Similarity 41.2%; Pred. No. 2e-83;
Matches 382; Conservative 125; Mismatches 248; Indels 172; Gaps 29;

QY 12 DSSSRREAPRRPPVGGEGTTPPCOPSYGKVOSTKPMFVS-----SN 54
DB 48 DLGASTEDAPRRPPVGGEGE-----LVSTDPRAASVFCSCGKVGIKGEMSTAT 97
QY 55 ARNEDGIG-EPEGRRSPSPPLTWTMTKSLHSLGGODCAVLTPTLENEKCVDTIDFMA 113
DB 98 PRRSOLDLCEPEGASAPRPPLKMAESLHSLDDDGSLFRTFLKOGCGADLIDFMA 157
QY 114 CNGFRQMLKDT--KTLVAKAIKRYI-ENNSVYSKQLPATKYTRDGIKKOIGSV 169
DB 158 CTGFRKLEPCDSNEEKRILKAIATYKTYLDNNGIVSQTKPATSFILKGLIMKOLIPA 217
QY 170 MFDQOTELQANMENAQVFLTSITYLEYVSGGEMTAWS--NGIGLSKVLGCVLPT 227
DB 218 MFDQOTELQATMENTYPSFLKSDILEYTRTGSESPKVSDDSGSGTGKIGSLYPT 277
QY 228 LNEEBEWT-----ADLKCLSPTVYGLSKTLRAFAVSRTETAENGFRFKR 276
DB 278 LNEDEEMKCDMDDEDDRDADAPRRL-PQKILLETAPRVSSRRISSEGEFRIGSWR- 335
QY 277 SDPVNPIYVGGSYFAPATSDSE--LSSDALTDMSMTDSDVGVPPRYMGSKQL 333
DB 336 -EPVNPYVYVNGYALAPATSDSE--LSSDALTDMSMTDSDVGVPPRYMGSKQL 389
QY 334 QREHMRSAKANGOVSLPHFRTHRLKREMTYPERAFAELISRLKLEKLESHSLSE 393
DB 390 RREMOESQVAVNGRPLPIPTTRTKYEVK-VEQKFAEELIHLLEAVORTREAEKLEE 448
QY 394 RLQOIREDEKESGEQALSHRDGAPVQ-----HPLALPSS-----G 429
DB 449 RLKRVMEEEGE-----DGDPSGSPRCFKLPRAPAMHFRPRLCTMACAGIRD 499
QY 430 SYEDPOTILDDHLSVLTKTPCCSPGVGRSPRSRBDHNNHNOQCHTLSTGSKL 489
DB 500 AHENPESILDEHVOYRLVTRTGROSPG-----PGRHSPDSGHV-----AKM 540
QY 490 PNVACPLLGSKFLTKQTKT-----HVNHHYIHHNAVPKTEELAEATQVRC 539
DB 541 PVALGGAASGHGKHVRPSGAKLDAAGLHHNHVHHV--HHSTARKPEQVBAETRAQS 598
QY 540 LCPGCTIYCYSK-----CSHPRARERLPEBOFCGSRGGLTPRRNAKGTERTALSARD 594
DB 599 SFWAGLEPHSHGARSRGYSVGAAPNADGLAHSG-KVGVACRKNRAKKAESGKAST-- 655
QY 595 GMSAAGPOLPG--EEGRSDPVWOMLSEBRO--SKSKPMSAQSTIKSYPLESARA 649
DB 656 -----EVRGASPDALKKNQIMOWITEGEKEISRHRTGHGSGTAKKPOPHENSRP 705
QY 650 APGERVSRHLLGASGHSVARAHPTODPAMPRLTPNTLAOLEBACRRLAEVSK-- 706
DB 706 -----LSLEHPMAGPOLRTSVQPSHLEIDOPTMRPHARPPLQLOLEARRRLLEEERAS 760
QY 707 --PQKQCCCAASOORNDNHNHSAAGASPPANP-----SLAPEDHKPEPKLASY 753
DB 761 RABSKQYVOEVMWR-----GRACVPRCAVYLHVPAVSDMELSETETRSQRKVGCG 813
QY 754 HALQASELVTVYFCEGEIEPYRRLKQSLTGLHFEQKSLKGNVYVYFKKASDEACGA 813
DB 814 SAQPCOSIYAVYFCGPPIYKRLVNGRAVTLLOQFELLTKKGSYRYFKVSDERDCG 873
QY 814 VFEIIMDETFLVPMYEGRLIGKVERID 840
DB 874 VFEVEDEAVLPEFEKIGKVEKVD 900

```

```

RESULT 11
AXN_DROME STANDARD; PRT; 745 AA.
ID AXN_DROME
AC Q9VA07; Q9XXC1;

```

```

DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE AXIN (AXIS INHIBITION PROTEIN) (DAXIN) (D-AXIN).
GN AXN OR CG7926.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=99174086; PubMed=10073940;
RA Hanada F., Tomoyasu Y., Takatsu Y., Nakamura M., Nagai S.-I.,
RA Suzuki A., Fujita F., Shibuya H., Toyoshima K., Ueno N., Akiyama T.;
RT "Negative regulation of Wingless signaling by D-axin, a Drosophila
RT homolog of axin.";
RL Science 283:11739-11742(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Ruel L., Anthopoulos N., Goncalves J., Manoukian A.S., Woodgett J.R.;
RT "A Drosophila homolog of the axin gene is involved in the transduction
RT of the wingless signal regulating the stability of the armadillo
RT protein.";
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceoliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner K., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
RA Brannon R.C., Rogers J.-H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheibel F., Shen H.,
RA Shue B.C., Siden-Kimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [4]
RP FUNCTION.
RA MEDLINE=99387984; PubMed=10457025;
RA Willert K., Logan C.Y., Atora A., Fish M., Nusse R.;
RA "A Drosophila Axin homolog, Daxin, inhibits Wnt signaling.";

```



```

RL Development 126:4165-4173(1999).
CC -1- FUNCTION: INHIBITOR OF THE Wg SIGNALING PATHWAY. DOWN REGULATES
CC BETA-CATENIN (ARMADILLO-ARM). PROBABLY FACILITATE THE
CC PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (ZESTE-WHITE
CC 3-2W3).
CC -1- SUBUNIT: INTERACTS WITH ZW3 AND ARM. THE INTERACTION BETWEEN AXN
CC AND ARM OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN ARM.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: UBIQUITOUSLY EXPRESSED THROUGHOUT THE
CC DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DIX DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF086811: AAD24866.1: -
DR EMBL: AF091813: AAF21293.1: -
DR EMBL: AE003772: AAE56993.1: -
DR FlyBase: FBgn0026597: Axn.
DR InterPro: IPR000342: -
DR InterPro: IPR001158: -
DR Pfam: PF00778: DIX.1.
DR PROSITE: PS50132: RGS.1.
DR Developmental protein.
FT DOMAIN 54 172 RGS.
FT DOMAIN 640 646 POLY-SER.
FT DOMAIN 663 745 DIX.
FT CONFLICT 454 454 R -> Q (IN REF. 1).
FT CONFLICT 644 645 MISSING (IN REF. 1).
SQ SEQUENCE 745 AA; 81718 MW; 31A502528CE84BA CRC64;

```

```

Query Match 10.38; Score 457.5; DB 1; Length 745;
Best Local Similarity 22.28; Pred. No. 8.9e-19;
Matches 212; Conservative 125; Mismatches 277; Indels 341; Gaps 39;

OY 13 PSSSFRED-----APRPVGEGETPPCQPSVGVKSTKPMYSSNMRNDEGGEDEG 67
DB 5 PSGRKRDNDNCGSRPPVPEE-----SRKKMTGEGADNSK 42
OY 68 RASPDSPLTRMTKSLHSLGDQDQAYLFRFLEREKCV-DTLDFWFCNGFRQNLKDT 125
DB 43 NSSPS--YLMNARTLNHLNEDRDGVELFKKYVEEAPAYNDHLNRYFACGELKQOT-DPE 99
OY 126 KTLVANAATIRYRIENNSVSKQLKPKATKTYIRGDIKQ--QIGSVAFDOAQETIQAVM 182
DB 100 KIKIIGICATYFFLRKSQSLISDDLRAQIK-----AIKTNPEIPLSHFIDPMQRHVEYTI 154
OY 183 EENAYOVLETDIYLEYR-----SG--CENTAVYNSNGGLGSLKVLGCVLPTLN 229
DB 155 RDNITPFLCESEMITIYIQMSAQOERCTSSGATGSGSAGSSGSSGLAGACALPPTTA 214
OY 230 EEE-----WTCADLKCKLSPTVVGGLSKTLRATASVSTE 265
DB 215 SGKQQLPOLVPPGAFINLPVSSVGPAGTCSASGSVYGPTSMASSSSISATDILPRSS 274
OY 266 T-----AENG-----FRSFKRSD 278
DB 275 TLPFLHEDSVLSLDDFEKVOHQEGGSLGSGVAGARADYPIRLTRDLLIAIOKRRL 334
OY 279 PVNPIVHVGSGVEAFAT-----SANDSE---LSDALDT-DSMSTDDSDGVPPYR 326
DB 335 EIRP-PGAHGVYVNPSTNTSTVSPNSKVDSEBASVSSGGRDSDTWISISSGMDGRPIYQ 393
OY 337 MGSKQLOREMHRSYKANGOV-SLPHFPRTNRL-PKEMTPVEPPAFAELISRLKLE-384
DB 394 RHSTESKATROSAMAKETNTPTQVIRPTQRLHNSHRLKEELVSLILPKLE----E 449

```

```

OY 385 LESHRSLEERLOQ-----IREDEKEGSEFOALSROGAPVONHLLPLPSGYEEDPOTI 438
DB 450 VKRKDLERARERNPAGALLTNERSSASDRFAF---ALREKAL-----DENDODI 500
OY 439 LDDHLSRYLKTTPGSCPSGVGRYSPRSRPNHNNHNNQOCTLLSTGKLPYVAAEPL 498
DB 501 LDQHYSRWMD--QTP-----HNSP-----GTMSP----- 523
OY 499 GKSFLTKQTKNNNNYNNHNNVAPKTEIEATQVRKLCRGGTDYCYCKSKSPK 558
DB 524 -----CP----- 525
OY 559 APEPLGDFGSGRGCTLPKRNKAGTERGLALSARDGSSAAGROPOLGEGGRSDPYW 618
DB 526 --PLP-----SKRRT-----ATHDSGVN-DCGMSISG----- 550
OY 619 QWMESEKSKSKP-HSAOSIRKSYPLESARAAP-----EVSRRHLLGASGHSRVA 671
DB 551 ---HSMKHSKMPDHSSCSRKLTKMKPMSMTDSCISMFADVTYKYK--DASSRSGS-- 602
OY 672 RAHPTQDPAMPRLTPPTTLAQLEACRRLAEVSKPQORCCV-----ASQQRNNSA 725
DB 603 -----STASKLEAKRRLD--EPRRSRYAQPMPOMHLSQOPLASFS 643
OY 726 AGOAGSPFANDSLAREDHKEPKKLASVHALQASELVYTPFGCEIPIRYRLKAQSLTL 785
DB 644 SSSGGSISL-----PHORPLPA-----KRPITVFSCEEPVRYRKIPQTOPTL 690
OY 786 GHFEKLSKGNRYRYFKKASDEFACGAVFEIIMDETVLVPEGRILGKERID 840
DB 691 RQFKYLRGRGHFRFFFTHCEDPDSPIQEIIVDSILPLFGKAKGYKPSD 745

```

```

RESULT 12
RGSE_MOUSE STANDARD: PRT: 547 AA.
AC P97492:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) (RAP1/RAP2 INTERACTING
DE PROTEIN).
GN RGS14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC JANOUEIX-LEROSEY I., Tavilian A., de Gunzburg J.;
RA Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U85055: AAB41893.1: -
DR MGD: MGI:1859709: RGS14.
DR InterPro: IPR000342: -
DR Pfam: PF00615: RGS.1.
DR PRINTS: PR01301: RGSPROTEIN.
DR PROSITE: PS50132: RGS.1.
KW Signal transduction inhibitor.

```

FT DOMAIN 67 184 RGS.
SQ SEQUENCE 547 AA: 59833 MW: FIDBF29E5336EF75 CRC64:

Query Match 4.4%; Score 195; DB 1; Length 547;
Best Local Similarity 23.3%; Pred. No. 0.00039;
Matches 125; Conservative 85; Mismatches 201; Indels 126; Gaps 27;

```

QY 39 SVGKQSTKPMVSSNARNEDGLGE-----PEGKASP-----DSPLTRWTKSLHSLIG 87
DB 20 SDGELTST-----AGSOAQEGRGSSLSIHSILPSGSPSPFSTDEQPVASMAQSFERRLLQ 73
QY 88 DODGAVLFTFLEKRCVDTLDFWACNGFRQMNKDKDTL-RVAKAIYKRIENNSVVS 146
DB 74 DPGGLAVFTFLEKFESEAENVTFWACERFQDIPASDTKQLOAEHNIYHEFLS-----S 128
QY 147 KQKPAAT---KTYIRDGKIKQOIGSVMFDOAQTEIOAVMEENAYQVFLSDIYLEYVRSG 203
DB 129 QALSPVNIIDROMLSEEVLAQRPDP-MFRAOQLOIFNLMKFDYSARFVKSPLVQECCLAE 187
QY 204 GENTAVMNGG--IGS-----LKVLCGYLPTLNEEF-----EWTCA-DLKCKLSPT 246
DB 188 AEGRLPRPGSSHLGSPDTAKKPKLPGKSLPLGVEELGOLPLAEGPCGRPLKSFRR 247
QY 247 VVG--LSSKTLR-ATASVSTETAENGFRSPFRS-DPVNRYHVGSG-----YV 290
DB 248 MTGGMNGLALRREGSGSLNSASLDGLFVAVSSKSEHRKSLGSESESRPGKCV 307
QY 291 FAPATSANDELSLDALTDMSMTDS-----SVDGVPYRMS-KKQLOREHMR 339
DB 308 YLPDGT-----SLALARPGLITRDMLAGICEKRGSLPDIKYVLVNEGKALVLDDQC 361
QY 340 SVKNGQVSLPHFRTHRLPKEMTPVEPAFAELISRLKLELSRHSLEERLQIR 399
DB 362 TVLADQEV-----RLENKIT-----FQELVGLERYVRISAKPTKRLQALPIL 406
QY 400 EDEKEG--SEQALSSRDG---APVOHPLALPSGSYEEDPQTLDDHLSRVETKPGCQ 453
DB 407 ---AKHGSLDQVVLHRRGEKQMDLETPEVSSVASQTLVLD--TPPAKMSSEARISPCR 461
QY 454 SPVGGRVSPRSRPHHHNNHQQCHTLSTGKRLPVVACPLGKSKSLT--KQT 508
DB 462 SQGCG--LPRQTKDHS-----LPPSSSLVLEDASSSTGNROT 497

```

RESULT 13

RGS3_HUMAN

ID RGS3_HUMAN

STANDARD:

PRT; 544 AA.

```

AC 008773:
DT 01-NOV-1997 (Rel. 35, Created).
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14).
GN RGS14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97312490; PubMed=9168931;
RA Snow B.E., Antonio L., Suggs S., Gutstein H.B., Siderovski D.P.;
RT "Molecular cloning and expression analysis of rat Rgs14."
RL Biochem. Biophys. Res. Commun. 233:770-777(1997).
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN, LUNG, AND
CC SPLEEN. LOW EXPRESSION HAS BEEN FOUND IN HEART, LIVER, SKELETAL
CC MUSCLE AND TESTIS.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.

```

This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```

DR EMBL: U92279; AAC53175.1; -.
DR HSP: P00778; ITAL.
DR InterPro: IPR00342; -.
DR Pfam: PF00615; RGS.1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KW Signal transduction inhibitor.
FT DOMAIN 67
SQ SEQUENCE 544 AA: 59491 MW: FF624BD2F593B4E CRC64;

```

Query Match 4.3%; Score 190.5; DB 1; Length 544;
Best Local Similarity 21.9%; Pred. No. 0.00069;
Matches 117; Conservative 79; Mismatches 185; Indels 153; Gaps 24;

```

QY 39 SVGKQSTKPMVSSNARNEDGLGE-----PEGKASP-----DSPLTRWTKSLHSLIG 87
DB 20 SDGELTST-----SGSOAQEGRGSSLSIHSILPSGSPSPFSTDEQPVASMAQSFERRLLQ 73
QY 88 DODGAVLFTFLEKRCVDTLDFWACNGFRQMNKDKDTL-RVAKAIYKRIENNSVVS 146
DB 74 DPGGLAVFTFLEKFESEAENVTFWACERFQDIPASDTKQLOAEHNIYHEFLS-----S 128
QY 147 KQKPAAT---KTYIRDGKIKQOIGSVMFDOAQTEIOAVMEENAYQVFLSDIYLEYVRSG 203
DB 129 QALSPVNIIDROMLSEEVLAQRPDP-MFRAOQLOIFNLMKFDYSARFVKSPLVQECCLAE 187
QY 204 GENTAVMNGG--IGSLKXLCGYLPTLNEEWTCDLKCKLSPT----- 245
DB 188 AEGRLPRPGSSHLGSPDP-----ARKRPLKPKGSLPLGVEELGOLPL 231
QY 246 -----TVVGLSKTLR-ATASVSTETAENGFRSPFRS-DPVNRYHVGSG- 288
DB 232 AEGRLPKSFRRMPGAVNSALRREGSGSLNSASLDGLFVAVSSKSEHRKSLGSE 291
QY 289 -----YFAPATSANDELSLDALTDMSMTDS-----SVDGVPYRMS 327
DB 292 GESESRPGKCVCCVLPDGT-----SLALARPGLITRDMLAGICEKRGSLPDIKYVLV 345
QY 328 G-SKQLOREHMRSVKANGQVSLPHFRTHRLPKEMTPVEPAFAELISRLKLELE 386
DB 346 GKEQKALVLDDQCTVLADEV-----RLENKIT-----FQELVGLERYVRISAK 390
QY 387 SRHSLEERLQIREDEKEG--SEQALSSRDG---APVOHPLALPSGSYEEDPQTLDD 440
DB 391 PTKRLQALPIL---AKHGSLDQVVLHRRGEKQVLDENLVSSVASQTLVLD--TLPD 445
QY 441 DILSRVTKLPQGGSPGVGRYSPRSRPHHHNNHQQCHTLSTGKRLPVVAA 494
DB 446 AKTRASSIPCRSGC--LPRQTKDHS-----LPPSSSLVLEDASSSTGNROT 478

```

RESULT 14

RGS3_HUMAN

ID RGS3_HUMAN

STANDARD:

PRT; 519 AA.

```

AC P49366:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 3 (RGS3).
GN RGS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96178495; PubMed=8602223;
RA Dreyer K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
RT "Inhibition of G-protein-mediated MAP kinase activation by a new
RL mammalian gene family."
RL Nature 379:742-746(1996).
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM.
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27655; AAC50394.1; -
DR HSSP: P49799; IAGR.
DR MIM: 602189; -
DR InterPro: IPR000342; -
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PRO1301; RGS; PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KM Signal transduction inhibitor.
FT DOMAIN 394 510
SQ SEQUENCE 519 AA; 56601 MW; FICFE3F27D4673A0 CRC64;

```

```

Query Match 4.3%; Score 189.5; DB 1; Length 519;
Best Local Similarity 32.0%; Pred. No. 0.00074;
Matches 49; Conservative 26; Mismatches 67; Indels 11; Gaps 4;
OY 56 RNEDGLGEPEGRA-----SPDS-PLTRMTKSLHSLGDODGAYLPRTFLEKECYDT 107
DB 361 RNESPGAPRPAKADKMKKSPSEALKNGESLEKLLVYKQAVQAFLETFSEEN 420
OY 108 LDFWPCNGFPMNLKDTKTLRAKAIYKRYENNSVSKOLKPKATKYIRNGIKQOIG 167
DB 421 LEFWLACDEFKFKVK-SQSKAMSKAKKIFAEYIAIQACEKVNLDSTREHTDNL--QSVT 477
OY 168 SWFDOAQTEIOAVMEENAYOVFLTSIDYLEYV 200
DB 478 RGFDFLAKRIFGLMEKDSYPRFLKSLDLDLI 510

```

```

RESULT 15
RGS2_HUMAN STANDARD; PRT; 211 AA.
AC P41220;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2) (G0/G1 SWITCH REGULATORY
DE PROTEIN 8).
GN RGS2 OR G0S8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE=94235158; PubMed=8179820;
RA Siderovski D.P., Heximer S.P., Forsdyke D.R.;
RT "A human gene encoding a putative basic helix-loop-helix
RT phosphoprotein whose mRNA increases rapidly in cycloneximide-treated
RT blood mononuclear cells."
RL DNA Cell Biol. 13:125-147(1994).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RA Baggaley C.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=95371353; PubMed=7643615;
RA Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W.,
RA Minden M.D., Siderovski D.P.;
RT "Differential expression of a basic helix-loop-helix phosphoprotein
RT gene, G0S8, in acute leukemia and localization to human chromosome
RT 1q31."
RL Leukemia 9:1291-1298(1995).
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACUTE MYELOGENOUS LEUKEMIA (AML)
CC AND IN ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).
CC -1- PPM: COULD BE PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY
CC PROTEIN KINASE(S).
CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13391; AAA20680.1; -
DR EMBL: L13463; AAC37587.1; -
DR EMBL: AL035407; CAB62512.1; -
DR HSSP: P49799; IAGR.
DR MIM: 600861; -
DR InterPro: IPR000342; -
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PRO1301; RGS; PROTEIN.
DR PROSITE: PS50132; RGS; 1.
KM Signal transduction inhibitor; Cell cycle; Phosphorylation.
FT DOMAIN 83 199
SQ SEQUENCE 211 AA; 24382 MW; EFPEAE47EF9AD8F CRC64;

```

```

Query Match 3.9%; Score 172.5; DB 1; Length 211;
Best Local Similarity 26.9%; Pred. No. 0.0021;
Matches 46; Conservative 24; Mismatches 72; Indels 29; Gaps 4;
OY 30 EGETPPCQPSVGVKQVS---TKMPVSSNARRNEDGLGEPEGASPDSPLETRMTKSLHSL 85
DB 50 QNSSTPGKPKTKGKSKQQAIFRSPDEAQL-----WSEAFDEL 87
OY 86 LGDDGAYLFRTFLEKECYDTLDFWPCNGFPMNLKDTKTLRAKAIYKRYENNSVY 145
DB 88 LASKYGLAFAFALFSECEENIEFWLACEDEFKTKR-SPOKSSKARKIYDFIKKAPK 146
OY 146 SKQLPATKTYIRNGIKQOIGSWFDOAQTEIOAVMEENAYOVFLTSIDY 196
DB 147 EINIDPOTKILIAONI--QEATSGCTTAOKRKYISLMENNSIPRLESEFY 195

```

Search completed: October 23, 2001, 11:04:19
Job time: 142 sec

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2001, 11:01:36 ; Search time 31.06 Seconds
(without alignments)
3578.114 Million cell updates/sec

Title: US-09-587-574-1
Perfect score: 4445
Sequence: 1 MSSAVLVTLPPSSSFRED.....DEVLPMEGRILGKERID 840

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1295	29.1	706	13	Q9PRP2 xenopus lae
2	736	16.6	147	4	Q9H3M6 homo sapien
3	208	4.7	235	4	Q9NS28 mus sapien
4	180	4.0	192	11	Q9JL23 mus musculu
5	180	4.0	297	11	Q9JL22 mus musculu
6	175.5	3.9	204	13	Q9I9D9 xenopus lae
7	175.5	3.9	872	5	Q9NGO0 drosophila
8	175.5	3.9	1175	5	Q9VCX2 drosophila
9	173.5	3.9	211	11	Q9JHX0 ratu
10	173.5	3.9	1510	5	Q61802 caenorabdi
11	172.5	3.9	829	5	Q9UB06 drosophila
12	172.5	3.9	1175	5	Q9XVX8 drosophila
13	168.5	3.8	211	11	Q9JL24 mus musculu
14	168	3.8	11	11	Q9JL25 mus musculu
15	166	3.7	209	4	Q9H1M2 homo sapien
16	163.5	3.7	533	5	Q22998 caenorabdi
17	162.5	3.7	980	4	Q9S387 homo sapien
18	157.5	3.5	998	5	Q9W3B8 drosophila
19	156.5	3.5	1208	4	Q9HCF8 homo sapien

20	155.5	3.5	3536	5	Q9VZ30 drosophila
21	153.5	3.5	1023	11	P70588 ratu
22	151	3.4	1150	3	Q99129 uscllago ma
23	151	3.4	2559	5	Q44381 drosophila
24	150.5	3.4	2472	4	Q9NS89 homo sapien
25	150	3.4	1032	11	Q9QX27 ratu
26	150	3.4	2207	5	Q9U0V2 leishmania
27	149	3.4	2506	4	Q9NS88 homo sapien
28	149	3.4	2559	5	Q44113 drosophila
29	148.5	3.3	413	5	Q9N817 trypanosoma
30	148.5	3.3	1380	5	Q77086 drosophila
31	148.5	3.3	2417	5	Q9VAS9 arabidopsis
32	148	3.3	684	10	Q9SG87 arabidopsis
33	148	3.3	1783	4	Q15038 homo sapien
34	148	3.3	1791	4	Q60382 homo sapien
35	148	3.3	2296	4	Q9UHA8 homo sapien
36	148	3.3	2559	5	Q9V7X3 drosophila
37	148	3.3	3851	4	Q43161 homo sapien
38	148	3.3	3926	4	Q9UPA5 homo sapien
39	147	3.3	1200	5	Q25388 loliigo peal
40	146	3.3	2752	4	Q9UQ35 homo sapien
41	145.5	3.3	1436	5	Q9VH03 drosophila
42	145	3.3	2237	5	Q9V122 drosophila
43	144.5	3.3	997	4	Q9Y4G1 homo sapien
44	144.5	3.3	1019	4	Q9Y4G7 homo sapien
45	144.5	3.3	1162	5	Q9VMB7 drosophila

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	706 AA.
ID	Q9PRP2			
AC	Q9PRP2			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	AXIN-RELATED PROTEIN.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodidae; Xenopus.			
CC	NCBI_Taxid=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=OVARY;			
RA	Itch K., Antipova A., Ratcliffe M., Sokol S.;			
RT	"Dishevelled transduces a signal by displacing GSK3 from axin-GSK3 complex."			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF140243; AAF22574.1; -.			
DR	InterPro; IPR000342; -.			
DR	InterPro; IPR001158; -.			
DR	Pfam; PF00778; DIX; 1.			
DR	PRINTS; PR01301; RGSPPROTEIN.			
DR	SMART; SM00021; DAX; 1.			
SO	SEQUENCE 706 AA; 79196 MW; C3D0AF0D9540F162 CRC64;			
Query Match	29.1%; Score 1295; DB 13; Length 706;			
Best Local Similarity	38.5%; Pred. No. 4,1e-86;			
Matches 327; Conservative 114; Mismatches 251; Indels 158; Gaps 24;				
OY	1 MSSAVLVTLPPSSSFREDARPPVPEEGETPPCPQSVKVGQSTKRPV---SSNARR 57			
DB	1 MSSAGVLCIPDPSGPIFRETSLRPVPCOE-----TNFKPEKFTMDSOHLKH 48			
OY	58 NEDGGEPEGRASPSPLTRKTKLSLSLGDGDGAYLRTFLERKCYDITLDFWACNGF 117			
DB	49 KEDFNREAGCVAHDSRSRWGRSLNLLDDODGATLFRMYLEGGLDILLTFWACNGF 108			
OY	118 ROMNLKDKTKTLVAKAIYKRYIENNSVSKOLKPATYTYIRDIKKQOIGSVMFDOAQTE 177			

```

Db      109 RAADPLEPTSKAKAYMYONSSAVSGRLKPTTRTQVKCKVKNHQNKTVPDQAOE 168
Oy      178 IQAVMEENAYQVFLTDILEYRSGGENTATMSNGSLGSLAVLGYLPTLMEBEWTCA 237
Db      169 IQRAMQEAFTSLQSDICEKTAI-GVEDSPPEPSPG-----LPTLDEDEFG-- 217
Oy      238 DLKCKLSPTVGL-----SKTLRATASVSTETAEENFRSFRKRDPAVNPVHSGYVF 291
Db      218 -----GLHFRSSGMKINRAFSRI-----PPRNRSHFRLEQTYQ-----F 255
Oy      292 APATSANDELSDALITDQSMSTSSVYGVPRYMGSKQLQRMHNSVKANGVSLPH 351
Db      256 ARAASTINDEISSDALTEDSMSTGSDVGLPYR--SKK--QREIHNSVANGKYSLDF 311
Oy      352 PPRTRHLPKEMTPVPAFAALISRLERKLELESRLSELRLOIREDEKESDAL 411
Db      312 VRTMRPRAEKMPSPRAEAAKLTALTEVKYKQDAEKEKLEKLOLKEEELIADYDIPS 371
Oy      412 SSRDCAVONHPLALLPSGSYEEDPQTILDLHSLVLTGPGCSPGVGYSPRSRSPDHH 471
Db      372 SSHE-----TVPGALEDPPQSLDDHVSRLKTP-----ANLSPRSOSP----- 411
Oy      472 QHHNHQOCHLLTSTGSKLPRVACPLGSKFLTKQTKVHNHNYIHHNAVPKTEIEA 531
Db      412 -----FYORKKGFOP-----AFSKQTSLSCHLR-----PKVPOGMEA 444
Oy      532 EATQVRCLECPGTDYCYCKSKSHKAPERLPBQFCGSGTGLPKRNKAGTEPGLALS 591
Db      445 TST-----LASELRSSVSQRLRSRK---PBGCTOPHPREGTSANAVLTT 487
Oy      592 ARDGMSSAAGPOLPGEGRSDQVQWMLSESRQSKSPHSAQSIKSYPLESANAP 651
Db      488 -----PUSPEDEAERNHSLQWVLDSAK-----LMKKHRETAIVTP 524
Oy      652 GERVSRHHLGASGRSVARAHPTODRAMPRLTPRTLAQLEACRRLAE---VSKPQ 708
Db      525 CRELKK-----ATHRAASOPAHPLFLODTSMPLTAPRTLDQLEARRRLVEDKRPKLH 578
Oy      709 KORCCVASQORDRNHSAAGAGASPANPSLAPDHKEPKKLASVHALQASELVVTFYC 768
Db      579 KSRCSVQSTTLKEKGTAE-SVPSGSGFTLKLS-DEQKTAKKPSS--BCPOGLAIIVYFC 634
Oy      769 GEELPYRMKKAOSLTGHEFQDLSKGNRYTKKASDEPACAVAEETIMDETIVLPMY 828
Db      635 GERIPYMRKEPSTLQEFKELLKSKSNKYYPKESHEFECNAVQVEVEDAVLPLF 694
Oy      829 EGRTIGKVER 838
Db      695 EKITICKVER 704

RESULT 2
Oy      09H3M6 PRELIMINARY; PRT; 147 AA.
AC      09H3M6;
DT      01-MAR-2001 (Tremblrel. 16, Created)
DT      01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE      01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE      CONDUCTIN (FRAGMENT).
GN      AXIN2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Nakamura Y., Furukawa Y., Takahashi M.;
RL      Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Takahashi M., Furukawa Y.;
RT      Identification of 3' UTR of Axin2."

```

```

RL      Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB052751; BAB19762.1;
FT      NON-TER 1
SQ      SEQUENCE 147 AA; 16771 MW; 324562918E7A577A CRC64;

Query Match
Best Local Similarity 94.6%; Score 736; DB 4; Length 147;
Matches 139; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy      694 LEACRRLAEVSKRPQKRCVSAQORDRNHSAAGASPANPSLAPDHKEPKKLASY 753
Db      1 LEACRRLAEVSKRPQKRCVSAQORDRNHSAATYQATFPSPSLAPDHKEPKKLGY 60
Oy      754 HALQASELVVTFYFCGEIEIPYRMLKAOSLTGHEFKQSLKGNRYRYFKKASDEPACGA 813
Db      61 HALQASELVVTFYFCGEIEIPYRMLKAOSLTGHEFKQSLKGNRYRYFKKASDEPACGA 120
Oy      814 VFEETIMDETIVLPMYEGRTIGKVERID 840
Db      121 VFEETIMDETIVLPMYEGRTIGKVERID 147

```

```

RESULT 3
Oy      09NS28 PRELIMINARY; PRT; 235 AA.
AC      09NS28;
DT      01-OCT-2000 (Tremblrel. 15, Created)
DT      01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT      01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE      REGULATOR OF G-PROTEIN SIGNALING 13.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang W., Wan T., Yuan Z., He L., Cao X.;
RT      "A novel regulator of G-protein signaling."
RL      Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF076642; AAF80227.1;
DR      InterPro; IPR000342;
DR      Pfam; PF00615; RGS; 1.
DR      PRINTS; PR01301; RGSBPROTEIN.
SQ      SEQUENCE 235 AA; 27582 MW; 973ABDE8EC7DE3D5 CRC64;

```

```

Query Match
Best Local Similarity 30.8%; Score 208; DB 4; Length 235;
Matches 56; Conservative 34; Mismatches 58; Indels 34; Gaps 6;

```

```

Oy      41 GKVOSTKPMVPVSSNARRN-----ED-----GLGPEGRASPDSPLTWTSTSL 82
Db      29 GKRETSKEAKIKAKERKNRLSLVQKPEFHEDTRSSGHLAKETRVSPEEAV-RWGSF 87
Oy      83 HSLLDGQDGAFLFRFLERKCVDTLDFWFAQNGFR-----QNNLKQTKTLRVAKATYK 136
Db      88 DKLLSHRDGLFAFTFLKTFESEENIEFWIACEDPKKSGPOQHLLK-----AKATYE 140
Oy      137 RYIENNSVSKQLKPAATYITIDGIRKQOIGSVMPDQATELQAVMEENAYQVFLTSDIY 196
Db      141 KFIQTDAPREVNLDRHTKEVTINSTITOPTLHS--FDAQSRVQLOMEDSYTRFLKSDIY 198
Oy      197 LE 198
Db      199 LD 200

RESULT 4
Oy      09JL23 PRELIMINARY; PRT; 192 AA.
AC      09JL23;
DT      01-OCT-2000 (Tremblrel. 15, Created)

```

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 3S.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 RN NCBI_TaxId=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C; TISSUE=KIDNEY;
 RX MEDLINE=20243574; PubMed=10779778;
 RA Relf K., Cyster J.G.;
 RT RGS molecule expression in murine B lymphocytes and ability to down-
 regulate chemotaxis to lymphoid chemokines.*;
 RL J. Immunol. 164:4720-4729(2000).
 DR EMBL: AF215669; AAF34626.1; --
 DR InterPro: IPR000342; --
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR ProDom: PD001580; --; 1.
 SQ SEQUENCE 192 AA; 22501 MW; BE6E0C1FE07952F CRC64;

Query Match 4.0%; Score 180; DB 11; Length 192;
 Best Local Similarity 28.2%; Pred. No. 1.4e-05;
 Matches 48; Conservative 31; Mismatches 67; Indels 24; Gaps 4;

OY 32 ETRPCOPSYGVKQSTKPM-PVSSNARNEDGLGEPGRASPDSPLTRMTKSLSLGDDOD 90
 DB 37 ESPGAPASKTKTKTSFPTSEEA-----LKMSESLKLLHRY 76
 OY 91 GAYLFRTFLERKCVDTLDFWFCNGFRQNLKDTLRLVAKAIYKRYIENNSVSKOLK 150
 DB 77 GLEVFQAFIRTEPSEENLEFWLACEDEKVKV-SQSKMAKAKKIFAEFIAIQACEKVND 135
 OY 151 PATKTYIRGCIKQOIGSVFDOAQTEIQAVMEENAYQVFLTSIDILEYV 200
 DB 136 SYTREHTKENL--QSITRCGCFDLAQRIRFGLMKDSYPRFLRSLDYLDI 183

RESULT 5
 OY 09JUL22 PRELIMINARY; PRT; 297 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING 3 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 RN NCBI_TaxId=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=20243574; PubMed=10779778;
 RA Relf K., Cyster J.G.;
 RT RGS molecule expression in murine B lymphocytes and ability to down-
 regulate chemotaxis to lymphoid chemokines.*;
 RL J. Immunol. 164:4720-4729(2000).
 DR EMBL: AF215670; AAF34627.1; --
 DR InterPro: IPR000342; --
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 DR ProDom: PD001580; --; 1.
 FT NON_TER 1
 SQ SEQUENCE 297 AA; 33683 MW; ADF80985150B525C CRC64;

Query Match 4.0%; Score 180; DB 11; Length 297;
 Best Local Similarity 28.2%; Pred. No. 2.5e-05;
 Matches 48; Conservative 31; Mismatches 67; Indels 24; Gaps 4;

OY 32 ETRPCOPSYGVKQSTKPM-PVSSNARNEDGLGEPGRASPDSPLTRMTKSLSLGDDOD 90
 DB 142 ESPGAPASKTKTKTSFPTSEEA-----LKMSESLKLLHRY 181
 OY 91 GAYLFRTFLERKCVDTLDFWFCNGFRQNLKDTLRLVAKAIYKRYIENNSVSKOLK 150
 DB 182 GLEVFQAFIRTEPSEENLEFWLACEDEKVKV-SQSKMAKAKKIFAEFIAIQACEKVND 240
 OY 151 PATKTYIRGCIKQOIGSVFDOAQTEIQAVMEENAYQVFLTSIDILEYV 200
 DB 241 SYTREHTKENL--QSITRCGCFDLAQRIRFGLMKDSYPRFLRSLDYLDI 288

RESULT 6
 OY 09JUL22 PRELIMINARY; PRT; 204 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE RGS4 PROTEIN.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxId=83355;
 RP SEQUENCE FROM N.A.
 RA Wu C., Zeng Q., Blumer K.J., Muslin A.J.;
 RT "RGS Protein Inhibits Xwnt-8 Signaling in Xenopus Embryonic Development.*"
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF263451; AAF70201.1; --
 DR InterPro: IPR000342; --
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS: PR01301; RGS-PROTEIN.
 SQ SEQUENCE 204 AA; 23167 MW; 31D80DAE6C38120A CRC64;

Query Match 3.9%; Score 175.5; DB 13; Length 204;
 Best Local Similarity 27.6%; Pred. No. 3.2e-05;
 Matches 42; Conservative 37; Mismatches 68; Indels 5; Gaps 3;

OY 61 GLEPEGRASPDSPLTRMTKSLSLGDDGAYLFRTFLERKCVDTLDFWFCNGFRQNL 120
 DB 41 GYKPPSQVRQDEVKKMAESLENLNNECGLAARFSLQSEINIDPFWACENYKXI 100
 OY 121 NKDTLRLVAKAIYKRYIENNSVSKOLKPATKTYIRGCIKQOIGSVFDOAQTEIQ 180
 DB 101 KTG-ARLPQAKIYEDFISVATKEVNDLSVTRFETSNIIQPTYST--FDEAQHKIFI 157
 OY 181 VMEENAYQVFLTSIDILEYV--SGGENTAYM 210
 DB 158 LMEKDSYRRFLKSKFYLDIVNLSSGASTYK 189

RESULT 7
 OY 09JUL22 PRELIMINARY; PRT; 872 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE REGULATOR OF G-PROTEIN SIGNALING Loco III.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Euryptera; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephypteroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxId=7227;
 RP SEQUENCE FROM N.A.
 RA Paulirana S.V., Zhao D., Bowles M.;

"Loco III a new transcript of the RGS gene loco.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF245455; AAF62552.1;
 DR Flybase; FBgn020278; loco.
 DR InterPro; IPR000342;
 DR InterPro; IPR003109;
 DR InterPro; IPR003116;
 DR Pfam; PF00615; RGS; 1.
 DR Pfam; PF02196; RBD; 1.
 DR PRINTS; PRO1301; RGSPTROTEIN.
 DR SMART; SM00390; GLOCO; 1.
 SQ SEQUENCE 872 AA; 96116 MW; 658386B560A9FB40 CRC64;

Query Match 3.9%; Score 175.5; DB 5; Length 872;
 Best Local Similarity 19.4%; Pred. No. 0.0023;
 Matches 166; Conservative 138; Mismatches 359; Indels 193; Gaps 36;

DB 123 VPKVLTTPAPSAIRASVAAGCAQDHG--CPSS---WAGSFEMLDAAAGMOTFSEFL 176
 OY 100 EREKCVDTLDFEACNGFQRMNLTDTLRVKA--IKRYTENNVS---VSKQLKPAT 153
 OY 177 KKEFAENITFTACERR--LLESEADRYAQAAREIFAKLANNSSDPVNVDSQARSIT 233
 DB 154 KTYIRDGIRKQOIGSVFMDQATEIQAWEENAVOVLTSDIYLYEYVSGGENTAYMSG 213
 DB 234 BEKLADAAPD-----IFAPAQKQIFSLMKFDSYGRFTRSDLYKSCVEAEKQNGLPYSG 287
 OY 214 -GLSLKVLGCLPTLNEEEMTCADLCKLSPTVYVGLSSKTLKATASVSTETENGFR 272
 DB 288 LDLDLTLNPHLGAFSKTKK--SASNAEDRRKSLPMHMKR--RSKSRDTEIADQMH 344
 OY 273 SFKRSDPNYPYVSGYEAFAPTSAN-----DSELSSDALTDMSMTDSSVDGVPEYR 326
 DB 345 ALMPRPV-PQN-----APLTSALKYCGQNSLDLHSSRSSLSFDA---GTATGG 393
 OY 337 MGSKQQLQREMHRSYKANGVSLPRPRTHLRPEMTEVERPAFAELLISREKLEBLE 386
 DB 394 OGASTESYVSLCRVILTDGATFI-----VOTRGEYTGELVERL-----LE 434
 OY 387 SRHSLEERLQRIREDEKESQALSSRDGAPVGHPLALBSGSEEDPQITLDDHLSRV 446
 DB 435 KRN-----LVYRYDIDVFGSTKSID-----VOOPSOILG-----KEVYIERVAFK 477
 OY 447 LKTPCQSPGVGRYSRSPDPDHHO-----HHHHOCHTL----- 483
 DB 478 LDLP--DPKV--ISVSKRPKKQLHEVIRPLISKNYMEQOYIMRTQYRIDLNQVPT 532
 OY 484 -----STGKLRPVACPLLGKSFLLKQTKVHHHHYIHHHAYPKT 525
 DB 533 MADGQRLIVWNSDFVGGGSSMPKOSKPKPLPOGHLELTAKVNEELASKA----- 588
 OY 526 KEETEAETORVRLCPGCTDYCYCKSKSHPKAPEPLRPGFQGSRG-----TLPKR 579
 DB 589 -----DAAASEKSRPV-----DLSMSKNEAPSETSLFERMRROQRGGINIPASKPLKL 638
 OY 580 NAKTEPGLIASRDGSSAAGPOLP-----GEGDRSQDVMQWMLSEERSKSKPSA 635
 DB 639 KKKSTSS--SQOSEEAATQAVADPKPIIAKLKAGVQLQ-----VTEVAHEHQDILL 689
 OY 636 QSIKSY--PLESARA-----PEGRYSRHHLLGASHSSV--ARAHPTQDPAPEPLT 686
 DB 690 EGLRRAQIARLEDORGTEINDELDFLKNENKLSAAVSKLRKVASLSPEVKVATP-- 746
 OY 687 PPNTLAOLEEACRLAEVSKPOKORCCVAAQOQDBNHSNPAQAQASPPAN--PSLAPBDH 744
 DB 747 -----TELPQAPRLSITRSQQPVSPKVVDOEPETDLPAATQ--DQTEAKAPPLPPKPV 800
 OY 745 KEPKRLASVHALQASELVVTFYFCGEELPYRRM-----LKAQSLTGLHFKEQLS 793
 DB 801 VLPKIPSMWGAAP-----TGNCKNYSFSPSKQVPTSPKEAKPGCTGFASKITLDLGRKSL 855

OY 794 KKNRYRYFKKASDEF 809
 DB 856 EAGSKCATLDEPSSSF 871

RESULT 8
 OYVCX2 PRELIMINARY; PRT: 1175 AA.

AC OYVCX2
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE LOCO PROTEIN.
 GN LOCO OR CG5248.
 OS Drosophila melanogaster (Fruit fly).
 OC Euarystola; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise J.R., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bokkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Butlis K.C., Busam D.A., Butler H., Catiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegyam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "the genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003739; AAF56033.1;
 DR HSSP; P49799; IAGR.
 DR FLYbase; FBgn0020278; loco.
 DR InterPro; IPR000342;
 DR InterPro; IPR003116;
 DR Pfam; PF00615; RGS; 1.
 DR Pfam; PF02196; RBD; 1.
 DR PRINTS; PRO1301; RGSPTROTEIN.
 DR SMART; SM00315; RGS; 1.
 SQ SEQUENCE 1175 AA; 129703 MW; 0B9811610122AC59 CRC64;

Query Match 3.9%: Score 175.5; DB 5; Length 1175;
 Best Local Similarity 19.4%: Pred. No. 0.00034;
 Matches 166; Conservative 138; Mismatches 35; Indels 193; Gaps 36;

40 VGVOSTKPMVSSNARNEDGLCEPRASPSDLTRMTKSLHSLGDODGAYLFRTFL 99
 426 VPKVLTTPAPPSATIASVAEAGADHG--CPSS---WAGFEHMLDADAGMFFSEFL 479
 100 EREKCVDTLDWFACNGRGMNLTKTILRAKA--TKRTIENNSV---VSKOLKPT 153
 480 KKEFSAENIYFTACERYR--LLESEADRYVAQAREIFAHLANNSSDPVNVDSQARSIT 536
 154 KTYINDGIKKQIGSVMFDOAQTEIOAVMEENAVOVFLTSDILEYVSGGENTAYMSG 213
 537 EKLDAAPD-----IFAPAKOKIFSLMKFDSYORFTRSDLYKSCVEAEQNOPLPSG 590
 214 -GLGLKVLGCVLPTLNEEENTCADLKCLPTVVGSLSKTLRATASVSTETAENGR 272
 591 LDLDLTLKTNHFLGAFSKLK--SASNAEDRRKSLPMMHRT--RSKSRDREIMADQH 647
 273 SFKRDPMNPHVSGYFAPATSAN-----DSELSDALTDMSKMTDSSVDCVPRK 326
 648 ALMPAPV-PON-----APLTASLKLVCQNSLSDLHSSRSSLSFSDA---STATGG 696
 327 MGSKQOLREMHRSVKANGQVSLPHFRTNRLPKEMTPVEPAFAAELISRLKLELE 386
 697 OGASTESVSLCRVILTDATTT-----VOTRPEYVGLERL-----LE 737
 387 SNHSLERLOQIREDEKESEALSRDGAQVQHPRLALPESYEDPOTLIDHLNRY 446
 738 KRN-----LVRYDYIVQSGSTKSID-----VQOPSOILAG-----KEVIERVAK 780
 447 LKTPCCSPGCVGRYSPRSRPHNHQ-----HHNHQCHTL----- 483
 781 LDLP--DPKV--ISVSKPKKQKHEVIRPLSKYNYKMEQOVIMRTQVPIDLNQPV 835
 484 -----STGKLRPVACRPLLGKSFLLKQTKTNVHNHNNHNAVPKT 525
 836 MADGRLRIWVNSDFOVGGSSMPKOSKPKRPLRGHLDELTKVFNELASKA---- 891
 526 KEIEAEATQRYRCLPGCTDYCYCSKSHPKADEPLRGEOFGCSRG-----TLPRK 579
 892 ----DAASEKRPV-----DLCMSKSNEARSETSSLEFRMRRODROGNTIPASKPLRL 941
 560 NAKTEPGLAISARDGSSAAGPOLP---GEEGDRSDVQWMLSEROSKSKPMSA 635
 942 KKKSTSS--SQOSEEAATTOAVADPKPIIAKLKAGVKLO-----VTERVAHQDELL 992
 636 OSIRKSY--PLESARAA-----PGEVSRNHLILGASGHSRV-ARAHFTODDPRMPLT 686
 993 ECLKRAQARLEDDQTEINFDLRPFELKKNELSAVSKLRVRSLSVSKVPATP--- 1049
 687 PNTLAOLEACRLAEVSKPOKORCVASQORDRNHNSAAGASPFAN--PSLAPEDH 744
 1050 -----TEIPQAPRRLSTIRSQOVPSPMKVDQDEPTELRAATQ--DOTEFAKAPRPLPKK 1103
 745 KEPKLASVHALQASSELVVTFFGCEELIRYM-----LKAOSLTLGHEKQOLS 793
 1104 VLRIPRSMNGVAP-----TGNYCNKSPSKQVPTSPKASKPGTFAKRIPLDLRKSLDE 1158
 794 KKGNTRYFKKASDEF 809
 1159 EAGSRCAIYLDPESSSF 1174

RESULT 9
 09JHXO PRELIMINARY: PRT: 211 AA.
 AC 09JHXO: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE REGULATOR OF G-PROTEIN SIGNALING PROTEIN 2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY; TISSUE=THORACIC AORTA SMOOTH MUSCLE;
 RA Grant S.L., Lassegue B., Griendling K.K.,
 RT "RGS2 regulates angiotensin II signaling in vascular smooth muscle.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF279918; AAF85981.1; -
 DR InterPro; IPR000342; -
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 SQ SEQUENCE 211 AA; 24323 MW; 84B5525CB41EA964 CRC64;

Query Match 3.9%: Score 173.5; DB 11; Length 211;
 Best Local Similarity 29.2%: Pred. No. 4.7e-05;
 Matches 50; Conservative 23; Mismatches 65; Indels 29; Gaps 6;

30 EGEPKPCPSVGK--VOST--KMPVSSNARNEDGLCEPRASPSDLTRMTKSLHSL 85
 50 QNSTPGRKPKTKGKQCFIKRSP-----EAL-----LMAEAFDEL 87
 86 LGDODGAYLFRFLERKCVDTLDWFACNGRGMNLTKTILRAKAIYKRTIENNSV 145
 88 LASKYGLAFAFLSEFCEENIEFWLACEDPKRK--SPQKSSKARKLYTDFIKEARK 146
 146 SKOLKATKYTRDGIKKQIGSVMFDOAQTEIOAVMEENAVOVFLTSDILEY 196
 147 EINIDPQTKTILAIQNI--QEAISGCTTAQKRYVSLMENSIPRLESSEFY 195

RESULT 10
 061802
 AC 061802: PRELIMINARY: PRT: 1510 AA.
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE H1LE01.3 PROTEIN.
 GN H1LE01.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Lattelle P.,
 RA Lightning J., Lloyd C., Mcmurtry A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smailton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.; III of C.
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Geisel C., Wamsley P.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;

RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF067222; AAC17017.1;
 SQ SEQUENCE 1510 AA; 166889 MW; C1C08ACBC606FF11 CRC64;

Query Match 3.9%; Score 173.5; DB 5; Length 1510;
 Best Local Similarity 18.1%; Pred. No. 0.00068;
 Matches 168; Conservative 122; Mismatches 339; Indels 299; Gaps 40;

```

QY 13 PSSFFEDAPRPVPEGEETPCPSVGKVOSTKPMVSSN-----ARRNEDGIG 63
DB 255 PTTTRRKOS-----NRLRPINPKRNVPTKPPAPVSLQITRLPPAKKPPASRG 306
QY 64 BEGRASDPSLPTMTKSLHSLGDGAYLRTLEEREKCVDTLDFWACNGFQNMILK 123
DB 307 RPSNKRQTTTTTTTTTSVS-----KSPQIS 332
QY 124 DTKTL-----RAKAIKYKIENNSVSKOLKPA-----TKTY 156
DB 333 DNTLPTLPSTVTKGRTFGAAAAAATAAIGTAIIMDTLIDKEPEPSPRPVLETKTF 392
QY 157 IR---DGIR-KQOIGSVFDOAQTEIQAVM---ENAYQVFLSDYL-----EYV 200
DB 393 DRTSPDGVQVDEVPPELIDKLADSEDEVEKLAQEEOEFIRQIQLDNADPSHGDE 452
QY 201 RSGGENTAYMNSGGLGSLKVLGCLPLTINEEEMTCA---DLCKLSPTVVGLSKTL 255
DB 453 DSDSE-----PEYAEEDREPLAVOYOLEHQVDVS----- 482
QY 256 RATASVSTETAENGFRSFKRSDPVNRPVHSGVAFAPATANSSELSDD---ALTDG 311
DB 483 -PTSNVTDOSPRE---MYQHSER-----SPALSPDASVESEHERPARSPPT 526
QY 312 MSMTDSVDGVV--PYMGSKKQOLREMHRSKANGVSLPHFPTNRLPREKMPVEFAA 369
DB 527 LVTEQSTEDAPESPEVNEVHHVQTEAQOSPVIVHSTHVEHFD--TH---DESPQSVL 581
QY 370 FAELISLEKLKLELRHLEERLOQIRP-----EEKSGEALSSRGAPVQH 421
DB 582 -----SVHGEGEREDHDEAPVLSVHTDHKAHSEDPVS---PVOS 620
QY 422 PLALLPSGSEYEDRP---TILDLHLSKVLKTPGCSQSPGVG--RYSPPRSRP---DH 469
DB 621 VHSSHASHEIDEPQSPVPSVHSHASHIEQELPLPSVASERVPASSELVQSENEH 680
QY 470 HHQ-HHHH-----QQCHTLISIGKLPVAAACPLLGKSFLLKQTTKHVHH 515
DB 681 HAEVHSHASEHIDEALPSVQSVHSHHDHRRSSPVASEPARSPVQSSRTSEHFR 740
QY 516 -----YIHHNAVPTKEIEAEATORVACLOPGTDVYCYKCKSH----- 556
DB 741 GEVPOSSSNQFSSSEHIEERKQSPVNOESVHSPHASEHREHREVPHPSPAASQEEFGR 800
QY 557 -PKAREPLRGEOF---CGSRGGLPKRNKAGTEBGLALS-----ARDGMS-- 599
DB 801 SPVSHPSVSEHFEHNEAQSPPVASQDEAARSPSVHSHASEHFEHNEHRODSPPASOE 860
QY 600 -AAGGPOL---PGEEDRODVQOMLSEERQSKSPHSAOSTIRKYPLESAARABGER 654
DB 861 KAASPSVHSHASEHSEHROEIOHSPAASONEAARSP-SVHSHASEHIEH---HGES 915
QY 655 V-----SRHLLASGSH-----SRSYARAHPTQO-----DP 680
DB 916 LQSPVASMSEHNNMAESSEYTTSEKEISPTSFSSHTSQDFQOQSNFVASERDRNSP 975
QY 681 AMPPLPPNTLAOLEACRLAEVSK--POKORC-CVAQO-----ORDRHSAAGAGAS 732
DB 976 TFESSVYMAAARPLSPAASHAEGARSPSEFERAPLSHQLSGLNLEHDDNSAVVBAQOE 1035
QY 733 PFANPSLAPEDHKEPKKLAVHALQASE 760
DB 1036 PATQSPITPLEQEGRFERAASVNSYQASE 1063

```

```

RESULT 11
Q90B06 PRELIMINARY; PRT; 829 AA.
AC Q90B06;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING LOCO C1.
GN LOCO OR CG5248.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99180581; PubMed=10079238;
RA Granderath S., Stollwerk A., Greig S., Goodman C.S., O'Kane C.J.,
RA Klammt C.;
RT "Loco encodes an RGS protein required for Drosophila glial
RL development 126:1781-1791(1999).
DR EMBL: AF130745; AAD24581.1; -.
DR HSP: P49799; IAGR.
DR FLYBase: FBgn0020278; loco.
DR Interpro: IPR003116; -.
DR Interpro: IPR003116; -.
DR Pfam: PF00615; RGS; 1.
DR Pfam: PF02196; RBD; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR ProDom: PD001580; -. 1.
DR SMART: SM00315; RGS; 1.
SQ SEQUENCE 829 AA; 91446 MW; 5C979C2E11B8FEFF CRC64;

```

Query Match 3.9%; Score 172.5; DB 5; Length 829;
 Best Local Similarity 19.1%; Pred. No. 0.00036;
 Matches 166; Conservative 136; Mismatches 349; Indels 217; Gaps 36;

```

QY 40 VGKVOSTKRPVPSNARNNDGIGEPGRASPSPLTRKTSLSHSLGDGAYLFRTEL 99
DB 80 VPKVLTTPAPPSALTASVAAGAAQDHG--CPSS---WAGSFERMLQDAAGQTFSEPL 133
QY 100 EREKCYDTLDFWACNGFQOMLKOTFTLRVAKA--YKRYIENNSV---VSKOLKPT 153
DB 134 KKEFSANETIYFWACERYR---LLESEADRYAQARELPKHLANNSSDVPVNDQARSLT 190
QY 154 KTYIRGCIKKQOIGSVFDOAQTEIQAVMEENAYQVFLTSDIYLEVRSGGENTAYMSG 213
DB 191 EEKLADAAADP-----IFAPAKOIFSLMKFDYQRFIRSDLYKSCVEAEQKNQPLPYSG 244
QY 214 -GLGSLKVLGCLPLTINEEEMTCA DLKCKLSPTVVGLSKTLKATAVRSIETANGRR 272
DB 245 LDLELLKTNFHHGAFSKLTK--SASNAEDRRKSLTPMHRKT--RKSXSDREIYAMDQH 301
QY 273 SFKRSPPVNPYHVGSGVAFAPATSAN-----DSELSDALTDSSMTDSSVDGVPPYR 326
DB 302 ALMPAPPV-PQN-----APLTSASLKVCGQNSLDHSSRSSLSFDA---GSTATG 350
QY 327 MGSKQLODEMHRSVANGOVSLPHFPTNRLPREKMPVEPAFAELISLEKLKLELE 386
DB 351 OGASTESVYSLGRVILLDTGATYI-----VQTRPEYVGEIVERL-----LE 391
QY 387 SRHLEERLQRIREDEKSGEQALSSRGARVQHPHALLPBGSEEDPQTTLDHLSRV 446
DB 392 KRN-----LVYPTVDVFGSTKSID-----VQPSQTLAG-----KEVIEERRVAFK 434
QY 447 LKTPGQSPGVGRYSRSPRSDHNDQ-----HHHQOCHTL----- 483
DB 435 LDLP---DPKV---ISVKSFRKKQMLHEVIRPLISKYINKKEQVQVIMRTQVPIDLNOPT 489

```

```
OY 484 -----STGKLRPVACRLGKSEFLTKQTTKHVHHYIHHNAVPT 525
DB 490 MADGRLRIWVNSDFVGGSSMPKQSKPKRLPGCHLDELTKVFNELASKA----- 545
OY 526 KEELIATATORVRLCLPGCTDYCYCSKSHPKAPRLPGEOFGSROGTLPKRNAKTE 585
DB 546 -----DAAASE-----KSRP-----VDLCMSKSNAPSESSLFE 575
OY 586 PGLALSARDGMSAAGPOL-----PGEGRSDQDVMQ-----WMLE 623
DB 576 -RMROORDGDNIPASKLPKLKKSTSSQOSEEAATQTVADPKPILAKAGVKQV 634
OY 624 SEROSKSPHSAOSIRKSY--PLESARA-----PGEVRSHNHLGASGRSV-ARAH 674
DB 635 TERVAEMODELLEGLKRAQLARLEDQRTETINFDLPDLKKNENISAIVSKLRVRSLS 694
OY 675 PFTODPAMPRLTPNTLAQLEBACRLAEVSKPQKORCCVASQQRNRHNSAAGASPF 734
DB 695 PVSKVPATP-----TEIQPAPRLSITRSQQPVSPMKVDEPETDLPATQ--DQTEF 745
OY 735 AN--PSLAPEDHKERPKLASVHALQASELVVTFPGCEETRYRRM-----LKAQ 781
DB 746 AKAPRPLPPKRVLPKPSNMGVAOP-----TGNYCNKYSKQVPSPKESKRGTPAS 800
OY 782 SLTLGHFKEOLSKKNRYRYFKKASDEF 809
DB 801 KIPLDLGRKSLSEAGSCAVILDEPSSSF 828

RESULT 12
O9YX8 PRELIMINARY; PRT; 1175 AA.
AC O9YX8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING LOCO C2.
GN LOCO OR CG5248.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OY NCBI_TaxID=7227;
R [1]
SEQUENCE FROM N.A.
RA MEDLINE=99180581; Pubmed=10079238;
RA Grandenath S., Stollewerk A., Greig S., Goodman C.S., O'Kane C.J.,
RA Klemmt C.;
RT "Loco encodes an RGS protein required for Drosophila glial
RT differentiation."
RL Development 126:1781-1791(1999).
DR EMBL: AF130744; AAD24580.1; -.
DR HSSP: P49799; IAGR.
DR FlyBase; FBgn0020278; loco.
DR InterPro: IPR003109; -.
DR InterPro: IPR003116; -.
DR InterPro: IPR003116; -.
DR Pfam; PF00613; RGS; 1.
DR Pfam; PF02196; RBD; 1.
DR SMART; SM00390; GOLoco; 1.
FT VARIANT 18 18 R -> S.
FT VARIANT 19 19 N -> K.
FT VARIANT 56 56 G -> E.
SQ SEQUENCE 1175 AA; 129802 MW; 8E344F7321DB30F5 CRC64;
```

Query Match 3.9%; Score 172.5; DB 5; Length 1175;
Best Local Similarity 19.1%; Pred. No. 0.00057;
Matches 166; Conservative 136; Mismatches 349; Indels 217; Gaps 36;

OY 40 VGVKOSTRPMVSSNARNEDGLGEPGRASPDSPILTMTKSLSHSLDQDQAVLFFRTFL 99
DB 426 VPKVLTTPAPSAITVASVAEGAQDHG--CPSS-----WAGSFEMLDADAQMCFSEFL 479

```
OY 100 EREKCVDTLDFWPAFCNGFRQNLKDTKTLRVAKA--IYKRYIENSV-----VSKOLKPAT 153
DB 480 KKEPSAENITFTACERR--LLESEADRYVAQAEIETAKHLANNSDPVANDQASLT 536
OY 154 KTYIRDGIRKQOIGSVNEDQATEIOAVEMNAOVFLTSDIYLEVYSGGENTAYNSNG 213
DB 537 EEKLADAPD-----IFAPQOKOIFSLMKRDSYORFTRSDLYSCVABEKNQDPLPSG 590
OY 214 -GLSLKYLGLPTLNEEEMTCADLKCLSPVYVGLSKTLRATASVSTETAEKNGFR 272
DB 591 LDLELLKTNFHLGAFSKLKR--SASNAEDRRKSLILPHNRKT--RSKSRDTEITADMQH 647
OY 273 SFKSSDPVNPYHVGSGYFAPATSAN-----DSLSLSDALTDMSMTDSSVQVPRYR 326
DB 648 ALMPAPV-PQN-----APLTASLKLVCQNSLSLHSSRSSLSFDA---GTATGG 696
OY 327 MGSKLOLREHMRSVKANGOVSLPHFRTNRLPKEMTVEPAFAELISRLKLELE 386
DB 697 QGASTESVYSLCRVILTDGATTI-----VQTRGETVGLVERL-----LE 737
OY 387 SRHSLERLQOIREDKEGSEQALSSRDGAPVONPLALLPSGTYEEDPOTILLDHLRV 446
DB 738 KRN-----LVPRYDVIYFGSTKSID-----VQPSQILAG-----KEVIERRVAFK 780
OY 447 LKTPGCSPGVGRVSPRSRDPDHHQ-----HHNHQCHTL----- 483
DB 781 LDLP--DPKV--ISVSKPKQOLHEVIRPLISKYNYMEQOVIYMRTOVPIDLNQVPT 835
OY 484 -----STGKLRPVACRLGKSEFLTKQTTKHVHHYIHHNAVPT 525
DB 836 MADGRLRIWVNSDFVGGSSMPKQSKPKRLPGCHLDELTKVFNELASKA----- 891
OY 526 KEELIATATORVRLCLPGCTDYCYCSKSHPKAPRLPGEOFGSROGTLPKRNAKTE 585
DB 892 -----DAAASE-----KSRP-----VDLCMSKSNAPSESSLFE 921
OY 586 PGLALSARDGMSAAGPOL-----PGEGRSDQDVMQ-----WMLE 623
DB 922 -RMROORDGDNIPASKLPKLKKSTSSQOSEEAATQTVADPKPILAKAGVKQV 980
OY 624 SEROSKSPHSAOSIRKSY--PLESARA-----PGEVRSHNHLGASGRSV-ARAH 674
DB 981 TERVAEMODELLEGLKRAQLARLEDQRTETINFDLPDLKKNENISAIVSKLRVRSLS 1040
OY 675 PFTODPAMPRLTPNTLAQLEBACRLAEVSKPQKORCCVASQQRNRHNSAAGASPF 734
DB 1041 PVSKVPATP-----TEIQPAPRLSITRSQQPVSPMKVDEPETDLPATQ--DQTEF 1091
OY 735 AN--PSLAPEDHKERPKLASVHALQASELVVTFPGCEETRYRRM-----LKAQ 781
DB 1092 AKAPRPLPPKRVLPKPSNMGVAOP-----TGNYCNKYSKQVPSPKESKRGTPAS 1146
OY 782 SLTLGHFKEOLSKKNRYRYFKKASDEF 809
DB 1147 KIPLDLGRKSLSEAGSCAVILDEPSSSF 1174

RESULT 13
O9JL24 PRELIMINARY; PRT; 211 AA.
AC O9JL24;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OY NCBI_TaxID=10090;
R [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=EMBRYO;
```

